



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 04:36 PM UTC

PDB ID : 9K0Z / pdb_00009k0z
EMDB ID : EMD-61959
Title : EF-G2 bound 70S ribosome complex of M. smegmatis
Authors : Sengupta, J.; Baid, P.
Deposited on : 2024-10-16
Resolution : 4.70 Å(reported)
Based on initial model : 5O61

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

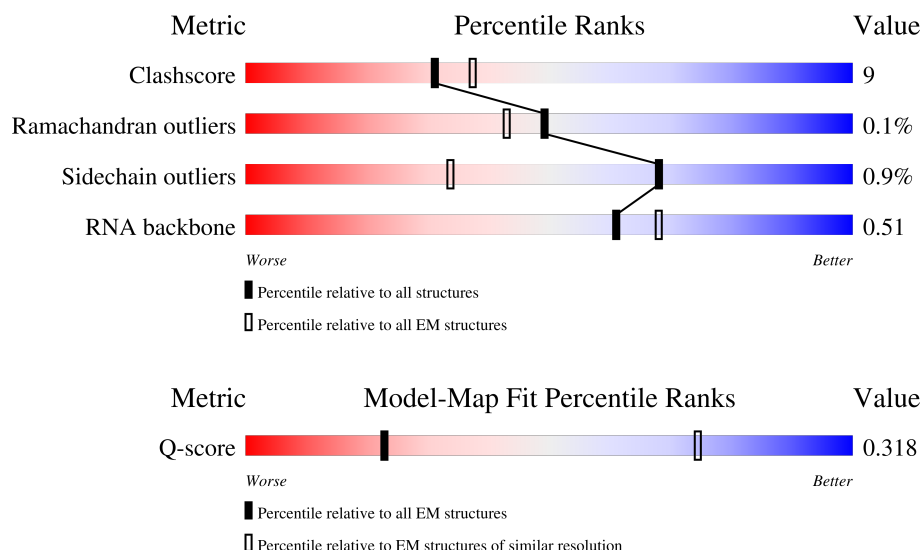
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1989 (4.20 - 5.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	2	76	
2	3	23	
3	4	18	

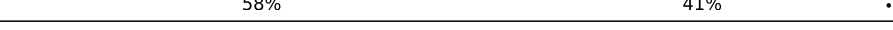
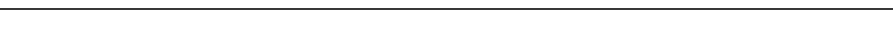
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Mol	Chain	Length	Quality of chain
4	5	69	
5	7	709	
6	A	1511	
7	B	118	
8	C	208	
9	D	200	
10	E	180	
11	F	96	
12	G	155	
13	H	131	
14	I	126	
15	J	99	
16	K	115	
17	L	122	
18	M	116	
19	N	60	
20	O	88	
21	P	113	
22	Q	94	
23	R	65	
24	S	82	
25	T	85	
26	U	97	
27	V	228	
28	W	192	

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Mol	Chain	Length	Quality of chain
29	X	79	 82% 18%
30	Y	63	 81% 19%
31	Z	64	 73% 27%
32	a	59	 76% 24%
33	b	54	 85% 15%
34	c	49	 67% 31% .
35	d	46	 76% 24%
36	e	63	 83% 17%
37	f	37	 84% 16%
38	g	48	 63% 38%
39	i	275	 80% 19% .
40	j	214	 81% 17% .
41	k	209	 85% 15%
42	l	182	 58% 41% .
43	m	176	 77% 23%
44	n	151	 79% 21%
45	o	126	 65% 35%
46	p	133	 62% 37% .
47	q	146	 81% 18% .
48	r	122	 77% 22% .
49	s	145	 82% 18%
50	t	136	 79% 21%
51	u	118	 79% 21%
52	v	126	 76% 23% .
53	w	113	 79% 21%

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Mol	Chain	Length	Quality of chain
54	x	124	 93%7%
55	y	100	 84%16%
56	z	114	 85%15%
57	l	105	 74%18%8%
58	h	3127	 61%31%6%•

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 155552 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called P/P-site Phe-tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	76	Total	C	N	O	P	0	0
			1614	721	287	531	75		

- Molecule 2 is a protein called 50S ribosomal protein bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 3 is a RNA chain called mRNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	18	Total	C	N	O	P	0	0
			390	176	80	117	17		

- Molecule 4 is a protein called Large ribosomal subunit protein bL12.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	5	69	Total	C	N	O	0	0
			505	321	83	101		

- Molecule 5 is a protein called Translation elongation factor EF-G.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	7	709	Total	C	N	O	S	0	0
			5299	3311	931	1039	18		

- Molecule 6 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	1511	Total	C	N	O	P	0	0
			32439	14448	5930	10550	1511		

- Molecule 7 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 8 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

- Molecule 9 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 10 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	180	Total	C	N	O	S	0	0
			1296	812	245	235	4		

- Molecule 11 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 12 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	155	Total	C	N	O	S	0	0
			1232	768	241	221	2		

- Molecule 13 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 14 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	I	126	Total	C	N	O	0	0
			994	630	194	170		

- Molecule 15 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	99	Total	C	N	O	S	0	0
			788	495	146	144	3		

- Molecule 16 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

- Molecule 18 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 19 is a protein called Small ribosomal subunit protein uS14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

- Molecule 20 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	O	88	Total	C	N	O	0	0
			720	449	147	124		

- Molecule 21 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	P	113	Total	C	N	O	0	0
			891	570	162	159		

- Molecule 22 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 23 is a protein called Small ribosomal subunit protein bS18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 24 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 25 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	T	85	Total	C	N	O	0	0
			660	402	139	119		

- Molecule 26 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 27 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 28 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	W	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 29 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 30 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 31 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 32 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	a	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 33 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 34 is a protein called Large ribosomal subunit protein bL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 35 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 36 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	63	Total	C	N	O	S	0	0
			502	302	115	85			

- Molecule 37 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 38 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 39 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 40 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 41 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 42 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 43 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 44 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 45 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 46 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 47 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 48 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 49 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 50 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 51 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 52 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	v	126	Total	C	N	O	S	0	0
			956	586	199	171			

- Molecule 53 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 54 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	x	124	Total	C	N	O	S	0	0
			988	613	203	172			

- Molecule 55 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	100	Total	C	N	O	S	0	0
			754	478	137	139			

- Molecule 56 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	z	114	Total	C	N	O	0	0
			873	543	171	159		

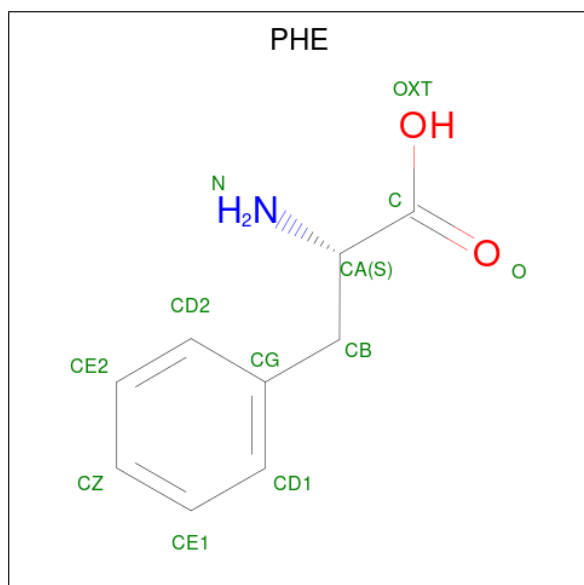
- Molecule 57 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	1	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 58 is a RNA chain called 23S ribosomal RNA.

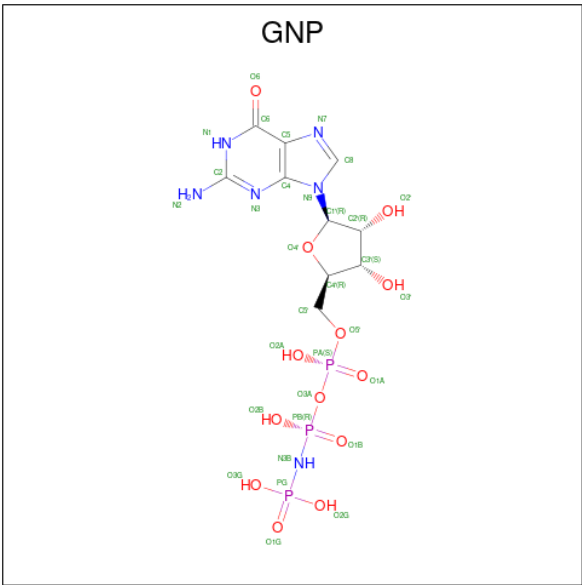
Mol	Chain	Residues	Atoms					AltConf	Trace
58	h	3071	Total	C	N	O	P	0	0
			65953	29397	12129	21356	3071		

- Molecule 59 is PHENYLALANINE (CCD ID: PHE) (formula: $C_9H_{11}NO_2$).



Mol	Chain	Residues	Atoms				AltConf
59	2	1	Total	C	N	O	0
			11	9	1	1	

- Molecule 60 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
60	7	1	Total	C	N	O	P	0
			32	10	6	13	3	

- Molecule 61 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
61	F	1	Total	Mg	0
			1	1	
61	R	1	Total	Mg	0
			1	1	
61	X	1	Total	Mg	0
			1	1	
61	i	3	Total	Mg	0
			3	3	
61	l	1	Total	Mg	0
			1	1	
61	t	1	Total	Mg	0
			1	1	
61	z	1	Total	Mg	0
			1	1	
61	h	3	Total	Mg	0
			3	3	

- Molecule 62 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
62	N	1	Total 1	Zn 1	0
62	R	1	Total 1	Zn 1	0
62	Y	1	Total 1	Zn 1	0
62	c	1	Total 1	Zn 1	0
62	f	1	Total 1	Zn 1	0
62	g	1	Total 1	Zn 1	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: P/P-site Phe-tRNA(Phe)

Chain 2: 



- Molecule 2: 50S ribosomal protein bL37

Chain 3: 



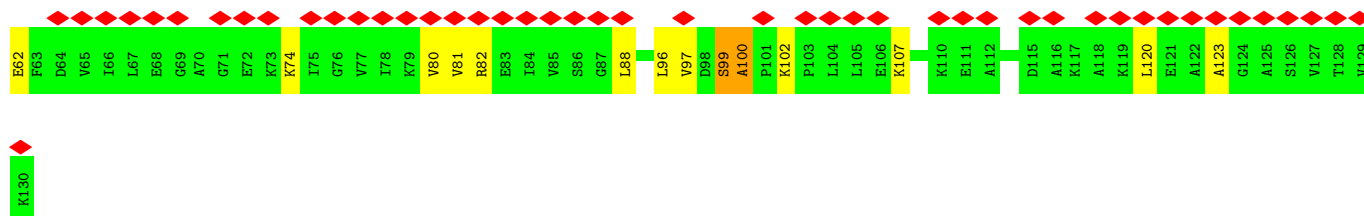
- Molecule 3: mRNA fragment

Chain 4: 



- Molecule 4: Large ribosomal subunit protein bL12

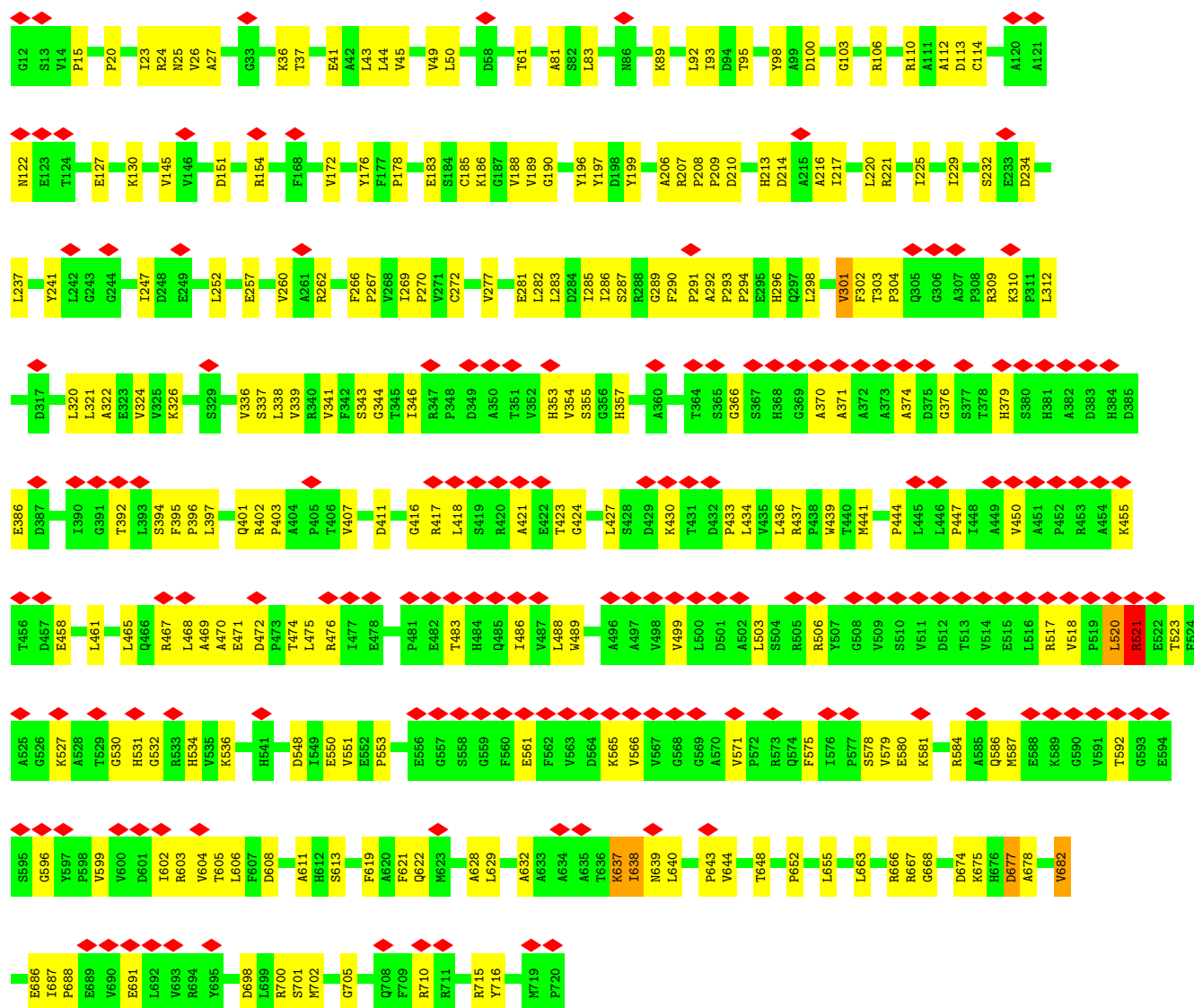
Chain 5: 

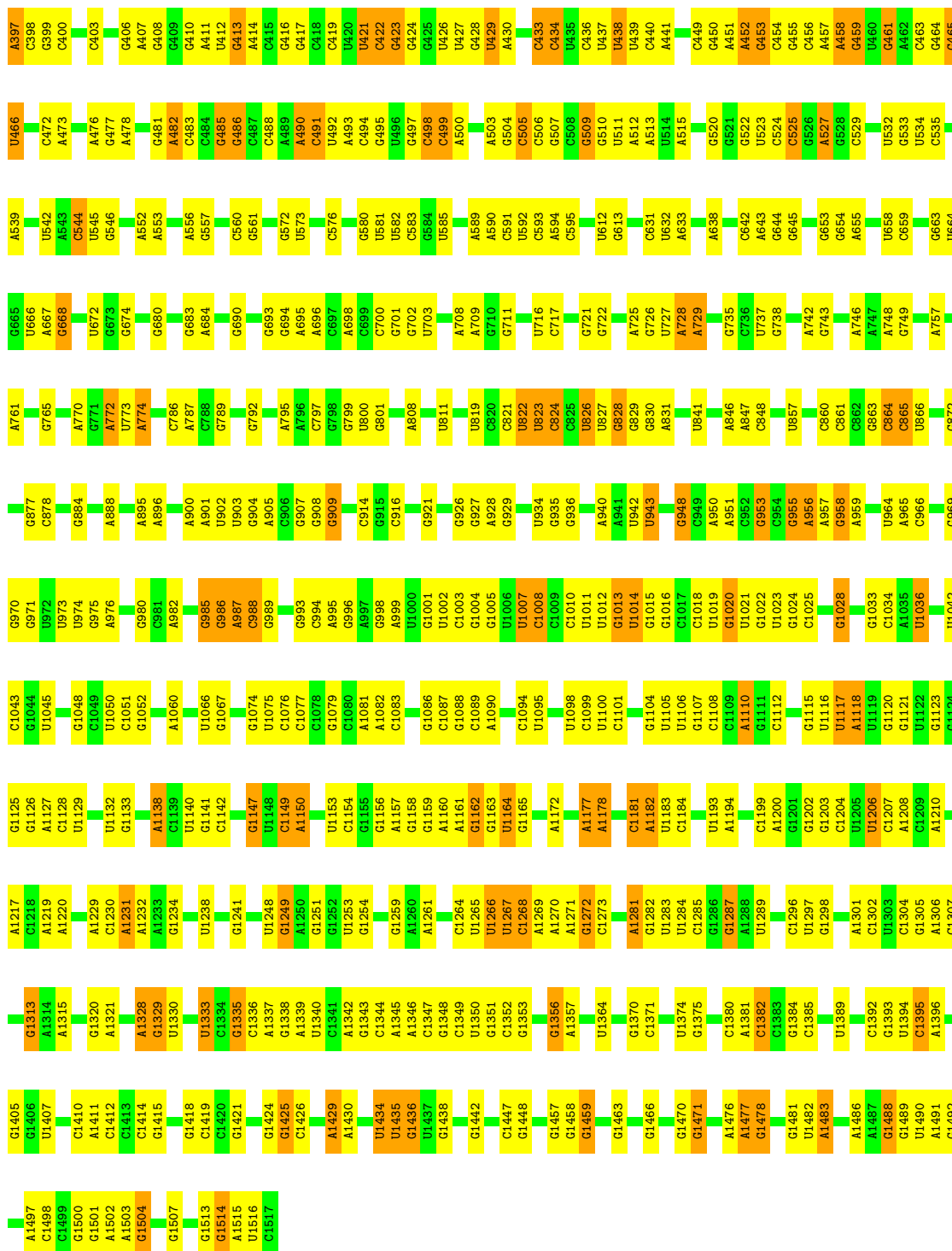


- Molecule 5: Translation elongation factor EF-G

Chain 7: 

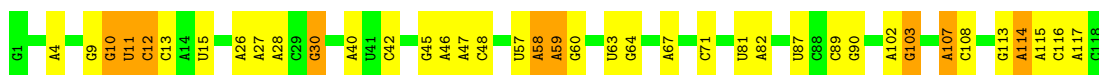






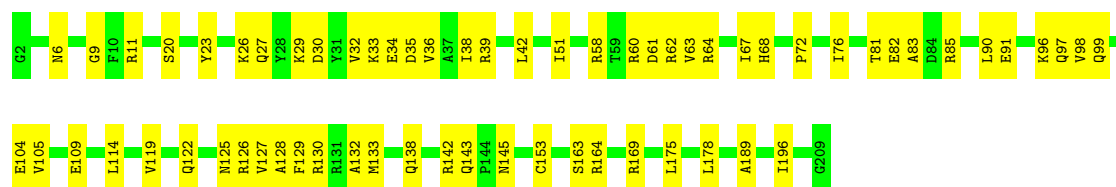
- Molecule 7: 5S ribosomal RNA

Chain B: 67% 25% 8%



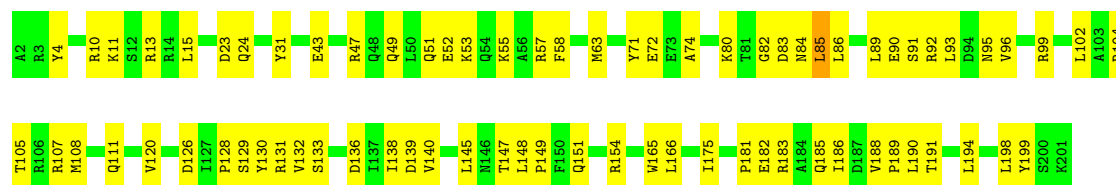
- Molecule 8: Small ribosomal subunit protein uS3

Chain C:  69% 31%



- Molecule 9: Small ribosomal subunit protein uS4

Chain D:  63% 36%



- Molecule 10: Small ribosomal subunit protein uS5

Chain E:  72% 28%



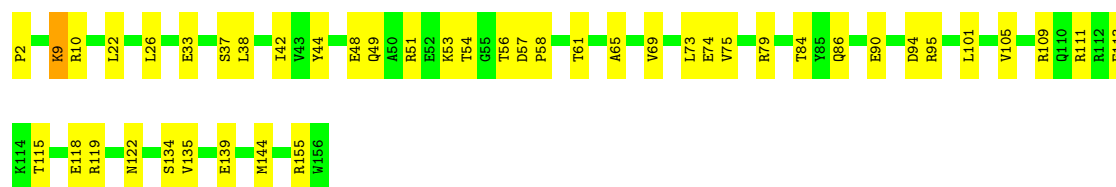
- Molecule 11: Small ribosomal subunit protein bS6

Chain F:  52% 47%



- Molecule 12: Small ribosomal subunit protein uS7

Chain G:  72% 28%



- Molecule 13: Small ribosomal subunit protein uS8

Chain H:  74% 26%



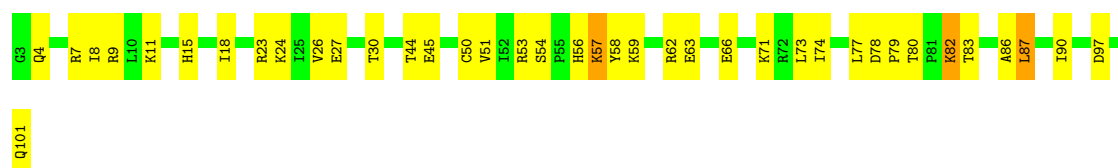
- Molecule 14: Small ribosomal subunit protein uS9

Chain I:  65% 34%



- Molecule 15: Small ribosomal subunit protein uS10

Chain J:  61% 36%



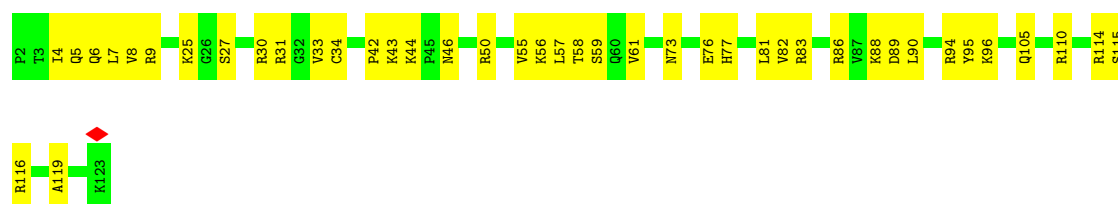
- Molecule 16: Small ribosomal subunit protein uS11

Chain K:  71% 28%



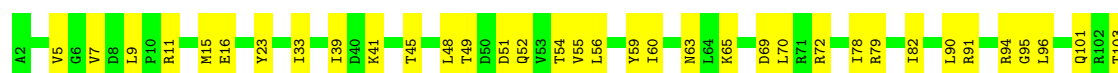
- Molecule 17: Small ribosomal subunit protein uS12

Chain L:  66% 34%



- Molecule 18: Small ribosomal subunit protein uS13

Chain M:  67% 33%





- Molecule 19: Small ribosomal subunit protein uS14B

Chain N: 73% 27%



- Molecule 20: Small ribosomal subunit protein uS15

Chain O: 73% 27%



- Molecule 21: Small ribosomal subunit protein bS16

Chain P: 66% 34%



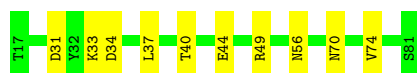
- Molecule 22: Small ribosomal subunit protein uS17

Chain Q: 60% 40%



- Molecule 23: Small ribosomal subunit protein bS18B

Chain R: 85% 15%



- Molecule 24: Small ribosomal subunit protein uS19

Chain S: 76% 23%



- Molecule 25: Small ribosomal subunit protein bS20

Chain T:  61% 38% .



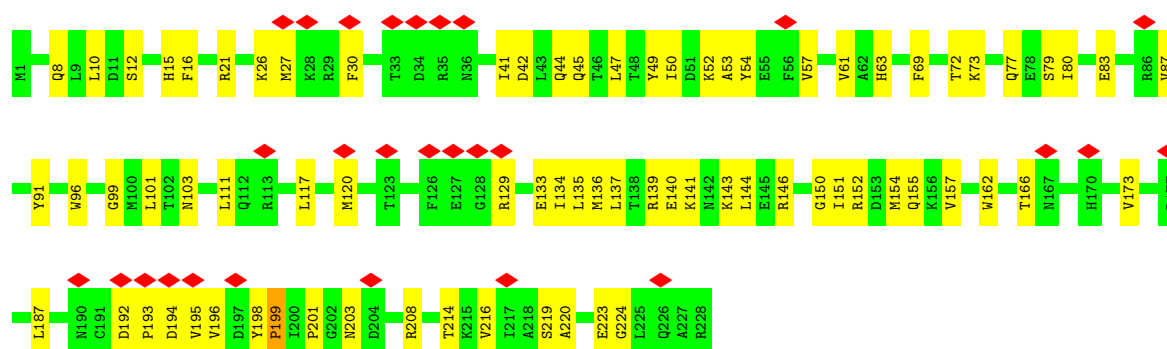
- Molecule 26: Large ribosomal subunit protein uL23

Chain U:  80% 20%



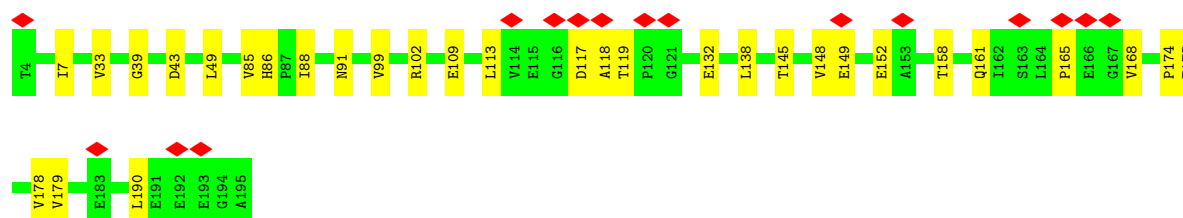
- Molecule 27: Small ribosomal subunit protein uS2

Chain V:  12% 67% 33%



- Molecule 28: Large ribosomal subunit protein bL25

Chain W:  8% 84% 16%



- Molecule 29: Large ribosomal subunit protein bL27

Chain X:  82% 18%

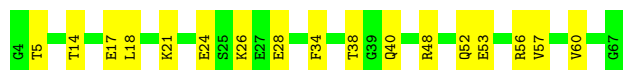


- Molecule 30: Large ribosomal subunit protein bL28

Chain Y:  81% 19%



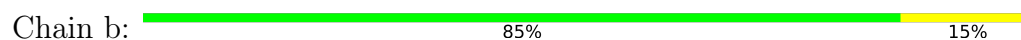
- Molecule 31: Large ribosomal subunit protein uL29



- Molecule 32: Large ribosomal subunit protein uL30



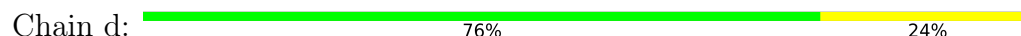
- Molecule 33: Large ribosomal subunit protein bL32



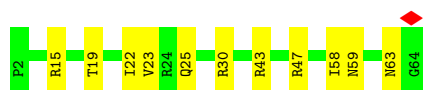
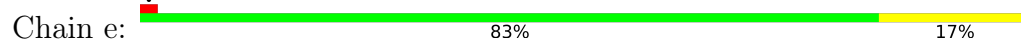
- Molecule 34: Large ribosomal subunit protein bL33A



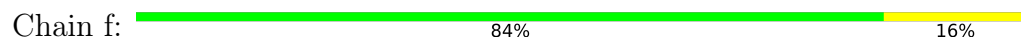
- Molecule 35: Large ribosomal subunit protein bL34



- Molecule 36: Large ribosomal subunit protein bL35

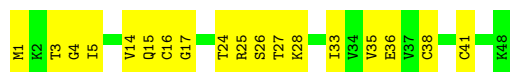


- Molecule 37: 50S ribosomal protein L36

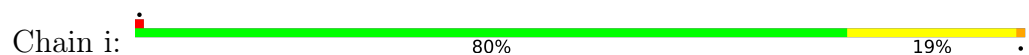




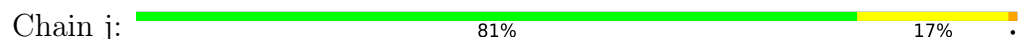
- Molecule 38: Large ribosomal subunit protein bL31



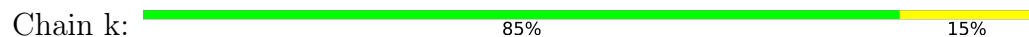
- Molecule 39: Large ribosomal subunit protein uL2



- Molecule 40: Large ribosomal subunit protein uL3

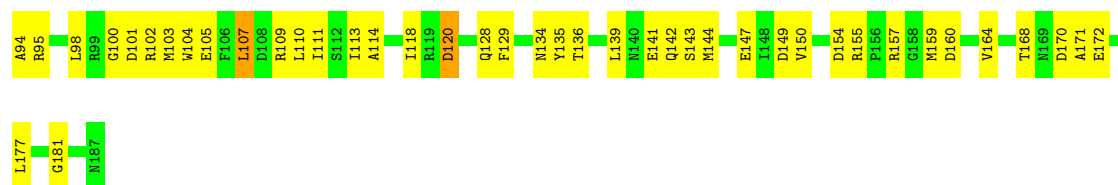


- Molecule 41: Large ribosomal subunit protein uL4



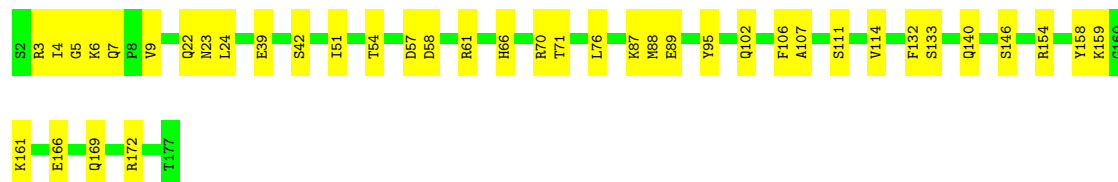
- Molecule 42: Large ribosomal subunit protein uL5





- Molecule 43: Large ribosomal subunit protein uL6

Chain m: 77% 23%



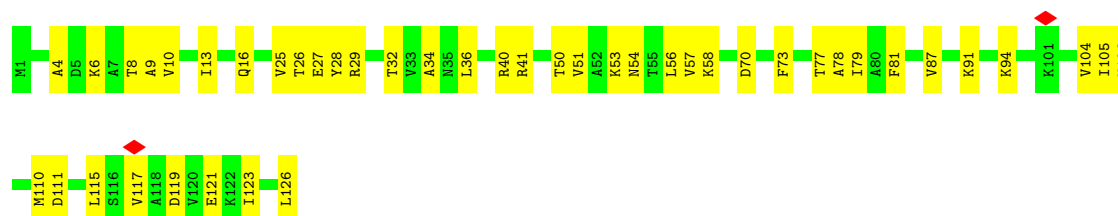
- Molecule 44: 50S ribosomal protein L9

Chain n: 79% 21%



- Molecule 45: Large ribosomal subunit protein uL10

Chain o: 65% 35%



- Molecule 46: Large ribosomal subunit protein uL11

Chain p: 62% 37%



- Molecule 47: Large ribosomal subunit protein uL13

Chain q: 81% 18%



- Molecule 48: 50S ribosomal protein L14

Chain r: 77% 22%



- Molecule 49: Large ribosomal subunit protein uL15

Chain s: 82% 18%



- Molecule 50: Large ribosomal subunit protein uL16

Chain t: 79% 21%



- Molecule 51: Large ribosomal subunit protein bL17

Chain u: 79% 21%



- Molecule 52: Large ribosomal subunit protein uL18

Chain v: 76% 23%



- Molecule 53: 50S ribosomal protein L19

Chain w: 79% 21%

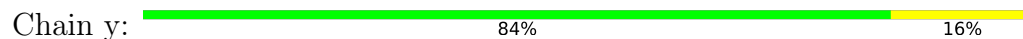


- Molecule 54: Large ribosomal subunit protein bL20

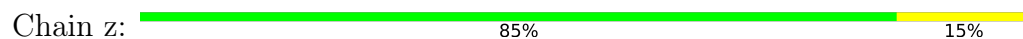
Chain x: 93% 7%



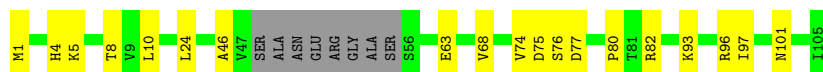
- Molecule 55: Large ribosomal subunit protein bL21



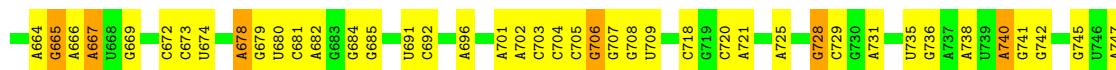
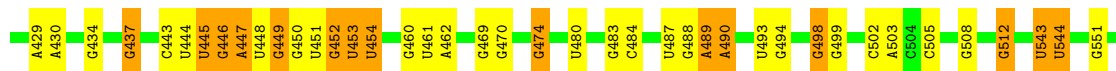
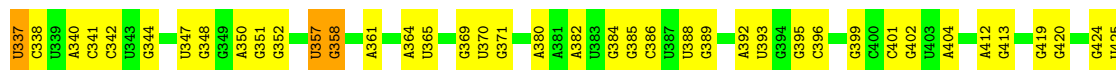
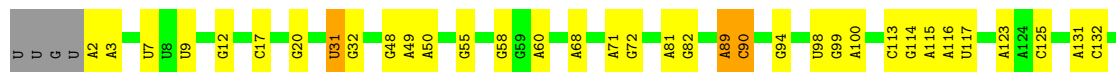
- Molecule 56: Large ribosomal subunit protein uL22



- Molecule 57: Large ribosomal subunit protein uL24



- Molecule 58: 23S ribosomal RNA



A2212	U2091	G1963	A1803	G1703	G	C1545	G1454	A1288	A1195	C1086	A976	U748
U2215	U2092	U1964	G1804	G1703	C	A1546	U1455	U1485	C1198	G1087	G977	C749
G2016	G2093	G1965	G1805	C1705	U	G1547	G1456	G1293	U1199	U1088	A978	C750
U2217	G2094	C1973	U1809	U1706	G	C1548	G1456	G1293	U1199	G878	G878	A751
A2221	G2095	A1974	A1810	G1707	C1610	G1549	C1465	C1298	U1200	G1092	U981	A879
	G2096	A1975	G1815	U1708	A1611	G1550	C1466	C1298	G1201	A1101	U981	A756
	G2097		G1815	U1709	U1612	U1551	U1467	G1326	A1202	A1101	G757	G757
	A2106	U1981	C1825	U1710	U1613	A1552	A1468	G1326	A1203	G1102	A758	A758
	G2107	A1990	A1826	G1711	G1614	U1554	A1469	G1334	A1204	G1102	G759	G759
				G1712	G1615	A1555	C1472	G1335	A1205	G1103	U760	U760
	U2110	U1996	G1840	U1713	A1616	A1556	G1473	G1335	G1207	C1112	U764	U764
	U2111			U1714		C1557	G1476	G1343	U1208	G1113	G895	G895
	U2112			A1715		C1558	A1344	A1344	G1209	G1114	G896	G896
	A2113	A2001	A1844	U1716			G1477	G1345	C1210	A1118	A897	A897
	A2114	A2003	U1854	U1717	G1622		C1478	G1345	G1211	A1119	A898	G767
			U1855	C1718	U1623		G1479	A1352	U1212	A1119	G768	G768
	A2125	C2007			U1624		A1480	G1353	C1001	C1125	U772	U772
	C2126	A2008	A1859	G1724	G1625		C1485	A1362	A1213	C1125	G773	G773
			G1860		U1626		G1486	A1362	A1214	C1130	G774	G774
	C2129	U2011	U1728	U1728	U1627			G1365	U1215	G1131	A904	A904
	G2130	C2012	A1729	A1729	U1628			G1365	C1220	A1131	A907	A907
			U1864	U1730	A1628			G1365	U1219	A1138	A908	A908
	A2136	G2016	C1865	A1731	G1629			G1365	C1221	A1144	U911	U911
	A2137	C2017	A1866	U1732	U1630			G1365	A1222	A1145	C912	C912
	C2138	G2018	G1867	C1733	A1631			G1365	C1223	A1146	A917	A917
	U2139	G2019	U1870	G1736	G1632			G1365	U1224	A1147	G920	G920
	A2140	A2019	A1871	U1737	G1639			G1365	U1225	A1147	G921	G921
	U2141	A2020	A1872	G1738	A1640			G1365	U1226	U1151	G922	G922
	A2142		U1877	A1739	G1642			G1365	C1227	G1157	G923	G923
	A2143	A2026						G1365	A1228	C1157	G924	G924
	C2144	U2033	U1877					G1365	U1229	A1164	U801	U801
	C2145	G2034	G1892	G1647	G1647			G1365	U1230	G1165	U818	U818
	A2146		C1893	A1648	A1648			G1365	U1231	G1165	G819	G819
	U2147	A2042	A1894	G1756	G1649			G1365	U1232	A1172	U829	U829
	C2148	C2043	A1895	U1757	G1650			G1365	U1233	G1174	A830	A830
		U2044		C1768	A1651			G1365	U1234	A1175	U942	U942
	G2153	G2045	C1900	G1762	A1652			G1365	U1235	G1176	A944	A944
	G2154	A2046	C1901	A1763				G1365	U1236	G1177	U847	U847
	A2160		C1904	A1764				G1365	U1237	U1178	G948	G948
	A2161	U2058	G1905	A1765	A1656			G1365	U1238	U1179	U954	U954
	A2162	G2059	G1905	U1766	G1657			G1365	U1239	G1180	C955	C955
	U2163	A2064	U1937	G1767	G1658			G1365	U1240	G1181	G960	G960
		A2065	G1938	A1680	A1659			G1365	U1241	A1050	U961	U961
	G2178	A2066	G1938					G1365	U1242	A1050	C964	C964
	U2179	A2070	G1942	U1781	G1670			G1365	U1243	A1050	U965	U965
	U2180	A2071	C1943	U1782	A1673			G1365	U1244	G1185	U862	U862
			C1944	G1786	U1675			G1365	U1245	A1186	G863	G863
	A2184	G2074	U1945	U1787	G1676			G1365	U1246	A1187	A864	A864
		G2075	U1946	A1788				G1365	U1247	A1188	A865	A865
	C2189	A2084	U1947	U1789	A1679			G1365	U1248	A1189	C888	C888
	A2190	U2086	A1948	A1790	A1680			G1365	U1249	C1190		
	C2191	C2085	G1950	A1791	U1681			G1365	U1250	A1191	A972	A972
		U2086	G1950					G1365	U1251	G1177	G973	G973
	A2194	C2087	G1951	U1798	A1690			G1365	U1252	A1184	C1081	C1081
	U2195	C2088	G1952		A1691			G1365	U1253	A1185	C1192	C1192
	G2196	C2089	C1953	C1801	A1691			G1365	U1254	A1186	C1193	C1193
				G1802				G1365	U1255	A1187	C1194	C1194
	C2211	U2090			G1696			G1365	U1256	A1188		



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	19431	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	54	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3300	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.090	Depositor
Minimum map value	-0.027	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.00715	Depositor
Map size (Å)	483.0, 483.0, 483.0	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GNP, MG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	2	0.15	0/1802	0.29	0/2807
2	3	0.25	0/191	0.33	0/247
3	4	0.13	0/439	0.27	0/684
4	5	0.17	0/507	0.41	0/678
5	7	0.15	0/5405	0.36	1/7360 (0.0%)
6	A	0.24	0/36309	0.31	0/56657
7	B	0.25	0/2821	0.27	0/4396
8	C	0.20	0/1684	0.48	1/2261 (0.0%)
9	D	0.25	0/1672	0.55	0/2251
10	E	0.26	0/1312	0.45	0/1772
11	F	0.24	0/782	0.45	0/1059
12	G	0.32	1/1252 (0.1%)	0.63	4/1690 (0.2%)
13	H	0.25	0/1025	0.42	0/1385
14	I	0.25	0/1012	0.51	2/1362 (0.1%)
15	J	0.24	0/802	0.49	0/1086
16	K	0.24	0/873	0.49	0/1180
17	L	0.27	0/969	0.50	0/1294
18	M	0.25	0/942	0.51	0/1260
19	N	0.25	0/488	0.42	0/650
20	O	0.24	0/729	0.36	0/977
21	P	0.25	0/908	0.48	0/1226
22	Q	0.26	0/759	0.57	0/1016
23	R	0.24	0/518	0.42	0/693
24	S	0.20	0/680	0.41	0/915
25	T	0.24	0/663	0.48	0/882
26	U	0.28	0/766	0.42	0/1030
27	V	0.21	0/1822	0.53	3/2457 (0.1%)
28	W	0.21	0/1443	0.37	0/1970
29	X	0.28	0/595	0.34	0/798
30	Y	0.33	0/478	0.36	0/641
31	Z	0.24	0/534	0.38	0/713
32	a	0.28	0/477	0.36	0/640

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.30	0/427	0.41	0/572
34	c	0.22	0/413	0.39	0/553
35	d	0.30	0/380	0.32	0/500
36	e	0.26	0/507	0.37	0/672
37	f	0.25	0/303	0.30	0/401
38	g	0.21	0/372	0.44	0/503
39	i	0.32	0/2153	0.42	0/2895
40	j	0.30	0/1609	0.40	0/2165
41	k	0.28	0/1592	0.40	0/2153
42	l	0.25	0/1467	0.51	0/1973
43	m	0.21	0/1369	0.37	0/1848
44	n	0.19	0/1027	0.43	0/1398
45	o	0.13	0/925	0.33	0/1246
46	p	0.17	0/1006	0.42	0/1364
47	q	0.29	0/1157	0.37	0/1567
48	r	0.28	0/946	0.42	0/1268
49	s	0.29	0/1091	0.45	0/1457
50	t	0.28	0/1118	0.42	0/1506
51	u	0.28	0/945	0.37	0/1267
52	v	0.25	0/966	0.41	1/1298 (0.1%)
53	w	0.28	0/921	0.42	0/1236
54	x	0.30	0/1000	0.34	0/1341
55	y	0.27	0/764	0.32	0/1030
56	z	0.28	0/887	0.37	0/1204
57	1	0.24	0/738	0.41	0/987
58	h	0.31	1/73851 (0.0%)	0.32	3/115230 (0.0%)
All	All	0.27	2/168593 (0.0%)	0.35	15/251671 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	h	2894	G	O3'-P	-12.13	1.43	1.61
12	G	2	PRO	N-CD	5.76	1.55	1.47

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	G	2	PRO	CA-N-CD	-13.91	92.53	112.00
58	h	2895	A	O3'-P-O5'	10.16	119.24	104.00
27	V	199	PRO	N-CD-CG	-9.20	89.41	103.20
12	G	2	PRO	N-CD-CG	-8.55	90.37	103.20
14	I	43	PRO	CA-N-CD	-7.98	100.83	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	h	2895	A	P-O3'-C3'	-6.50	110.45	120.20
27	V	199	PRO	CA-N-CD	-6.00	103.60	112.00
5	7	521	ARG	N-CA-C	5.39	117.71	109.95
8	C	60	ARG	CB-CA-C	-5.35	109.95	117.23
14	I	43	PRO	N-CD-CG	-5.32	95.23	103.20
52	v	5	PRO	CA-N-CD	-5.30	104.58	112.00
12	G	9	LYS	CA-C-N	5.26	127.96	120.49
12	G	9	LYS	C-N-CA	5.26	127.96	120.49
27	V	157	VAL	CA-CB-CG2	5.11	119.08	110.40
58	h	2085	C	C2'-C3'-O3'	5.02	117.02	109.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	1614	0	823	19	0
2	3	189	0	205	5	0
3	4	390	0	198	6	0
4	5	505	0	545	10	0
5	7	5299	0	5230	181	0
6	A	32439	0	16321	470	0
7	B	2522	0	1285	19	0
8	C	1660	0	1707	47	0
9	D	1641	0	1668	66	0
10	E	1296	0	1360	36	0
11	F	771	0	797	31	0
12	G	1232	0	1282	31	0
13	H	1010	0	1046	23	0
14	I	994	0	1050	35	0
15	J	788	0	819	33	0
16	K	855	0	863	24	0
17	L	958	0	1045	42	0
18	M	935	0	986	31	0
19	N	477	0	499	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	O	720	0	760	18	0
21	P	891	0	935	31	0
22	Q	748	0	795	31	0
23	R	513	0	537	8	0
24	S	662	0	677	13	0
25	T	660	0	712	27	0
26	U	756	0	802	12	0
27	V	1793	0	1839	54	0
28	W	1428	0	1443	18	0
29	X	586	0	601	11	0
30	Y	470	0	480	8	0
31	Z	531	0	541	12	0
32	a	474	0	500	8	0
33	b	423	0	463	8	0
34	c	405	0	407	13	0
35	d	377	0	411	7	0
36	e	502	0	541	11	0
37	f	299	0	321	6	0
38	g	364	0	348	14	0
39	i	2110	0	2165	38	0
40	j	1587	0	1630	32	0
41	k	1569	0	1607	24	0
42	l	1445	0	1476	54	0
43	m	1348	0	1399	31	0
44	n	1018	0	988	25	0
45	o	918	0	959	31	0
46	p	990	0	1021	38	0
47	q	1130	0	1167	23	0
48	r	938	0	1000	20	0
49	s	1078	0	1151	20	0
50	t	1092	0	1128	18	0
51	u	928	0	972	15	0
52	v	956	0	991	21	0
53	w	907	0	938	17	0
54	x	988	0	1038	6	0
55	y	754	0	802	8	0
56	z	873	0	909	12	0
57	1	732	0	782	13	0
58	h	65953	0	33183	675	0
59	2	11	0	8	0	0
60	7	32	0	13	2	0
61	F	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	R	1	0	0	0	0
61	X	1	0	0	0	0
61	h	3	0	0	0	0
61	i	3	0	0	0	0
61	l	1	0	0	0	0
61	t	1	0	0	0	0
61	z	1	0	0	0	0
62	N	1	0	0	0	0
62	R	1	0	0	0	0
62	Y	1	0	0	0	0
62	c	1	0	0	0	0
62	f	1	0	0	0	0
62	g	1	0	0	0	0
All	All	155552	0	106169	2267	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (2267) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:60:G:H4'	52:v:12:GLU:HG3	1.42	0.98
58:h:3013:C:H5'	58:h:3014:A:H5'	1.49	0.92
6:A:993:G:H1	6:A:1002:U:H3	1.14	0.89
58:h:1211:G:H21	58:h:1216:A:H62	1.19	0.86
58:h:2528:G:H22	58:h:2536:U:H3	1.20	0.85
6:A:483:C:OP1	17:L:116:ARG:NH1	2.10	0.84
6:A:1392:C:O2	58:h:2137:A:N6	2.10	0.84
6:A:772:A:O2'	6:A:774:A:N7	2.11	0.84
5:7:536:LYS:HE3	6:A:1478:G:H5'	1.59	0.83
43:m:57:ASP:OD1	43:m:58:ASP:N	2.11	0.83
58:h:1208:U:H3	58:h:1220:C:H1'	1.42	0.83
6:A:1014:U:H2'	6:A:1015:G:H8	1.44	0.82
26:U:67:LYS:HE2	26:U:76:ARG:HH21	1.43	0.81
37:f:31:ARG:NH2	58:h:2753:G:N7	2.27	0.81
58:h:334:G:H1	58:h:347:U:H3	1.26	0.81
9:D:43:GLU:HA	9:D:47:ARG:HH21	1.43	0.81
44:n:115:ARG:NH2	58:h:163:U:O2	2.13	0.81
41:k:198:VAL:O	41:k:202:ASN:ND2	2.15	0.80
6:A:1232:A:H62	6:A:1268:C:H42	1.28	0.80
57:1:75:ASP:OD1	57:1:76:SER:N	2.14	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:p:114:LYS:O	46:p:118:LEU:HB2	1.81	0.80
10:E:176:GLU:OE1	10:E:198:ARG:NH2	2.14	0.79
22:Q:23:ALA:HB1	22:Q:40:LEU:HD11	1.64	0.79
46:p:114:LYS:NZ	58:h:1177:G:O2'	2.12	0.79
58:h:289:A:H62	58:h:299:G:H22	1.28	0.79
58:h:1187:A:H4'	58:h:1188:A:H5''	1.65	0.79
6:A:1210:A:OP2	18:M:114:LYS:NZ	2.15	0.79
58:h:302:U:O2'	58:h:303:G:N7	2.15	0.79
21:P:49:ILE:HD12	21:P:73:LEU:HD22	1.65	0.78
12:G:9:LYS:NZ	12:G:10:ARG:O	2.15	0.78
8:C:35:ASP:OD1	8:C:58:ARG:NH2	2.17	0.77
33:b:45:LYS:NZ	58:h:3103:A:O3'	2.17	0.77
6:A:1421:G:OP2	25:T:29:ARG:NH1	2.16	0.77
6:A:1476:A:H2'	6:A:1477:A:H2'	1.67	0.77
5:7:441:MET:HE1	5:7:474:THR:HA	1.67	0.77
6:A:522:G:OP1	9:D:10:ARG:NH2	2.18	0.77
58:h:993:G:N2	58:h:1015:A:OP2	2.15	0.77
58:h:1825:C:N4	58:h:1840:G:OP2	2.18	0.76
5:7:110:ARG:HG3	5:7:439:TRP:HB3	1.64	0.76
6:A:728:A:O2'	6:A:729:A:N7	2.17	0.76
39:i:266:LYS:NZ	58:h:2448:G:OP1	2.18	0.76
58:h:1556:A:N1	58:h:1615:G:O6	2.18	0.76
48:r:112:MET:HA	48:r:112:MET:HE3	1.66	0.76
31:Z:21:LYS:NZ	31:Z:53:GLU:OE2	2.18	0.76
58:h:2340:A:H61	58:h:2389:U:H3	1.31	0.76
6:A:505:C:OP2	17:L:88:LYS:NZ	2.15	0.75
6:A:1486:A:H2	6:A:1489:G:H1	1.34	0.75
48:r:73:ASP:OD1	48:r:75:SER:OG	2.05	0.75
58:h:1544:U:H3	58:h:1626:G:H1	1.34	0.75
58:h:1001:C:H1'	58:h:1007:G:H22	1.52	0.74
21:P:86:LEU:HB2	21:P:87:PRO:HD3	1.68	0.74
38:g:36:GLU:OE1	38:g:36:GLU:N	2.19	0.74
58:h:365:U:H3	58:h:437:G:H1	1.32	0.74
58:h:2085:C:O2'	58:h:2086:U:O5'	2.05	0.74
58:h:1186:G:H21	58:h:1213:A:HO2'	1.34	0.74
30:Y:24:ARG:NH1	58:h:469:G:OP1	2.21	0.74
28:W:178:VAL:HG12	28:W:179:VAL:HG23	1.70	0.74
4:5:96:LEU:HD12	4:5:102:LYS:HE2	1.70	0.73
5:7:592:THR:HG22	5:7:638:ILE:HG21	1.70	0.73
39:i:258:ARG:NH1	58:h:2016:G:OP1	2.21	0.73
6:A:953:G:HO2'	6:A:1348:G:HO2'	1.24	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:58:ARG:HG3	8:C:63:VAL:HG22	1.71	0.73
5:7:312:LEU:HD12	5:7:321:LEU:HB2	1.71	0.73
6:A:1011:U:O2'	6:A:1013:G:N2	2.22	0.73
44:n:100:VAL:O	44:n:104:ILE:HD12	1.89	0.73
58:h:2342:A:N6	58:h:2390:U:O2'	2.21	0.73
6:A:644:G:H22	6:A:721:G:H1	1.34	0.73
18:M:79:ARG:NH2	58:h:1003:A:N1	2.36	0.73
51:u:106:ASP:OD2	58:h:1867:G:O2'	2.06	0.73
6:A:472:C:H2'	6:A:473:A:C8	2.23	0.73
6:A:653:G:H2'	6:A:654:G:C8	2.23	0.73
30:Y:41:ARG:HG3	30:Y:43:GLY:H	1.53	0.73
58:h:1188:A:N7	58:h:1214:A:O2'	2.21	0.73
58:h:1530:G:N2	58:h:1805:G:H1	1.87	0.73
6:A:1425:G:H5'	6:A:1426:C:H5	1.55	0.72
11:F:9:ILE:HD12	11:F:87:ARG:HB3	1.70	0.72
52:v:34:GLU:HG2	52:v:35:VAL:HG23	1.71	0.72
5:7:648:THR:HB	5:7:710:ARG:HB2	1.72	0.72
58:h:1186:G:N2	58:h:1213:A:O2'	2.15	0.72
58:h:981:U:O2'	58:h:982:A:OP2	2.07	0.72
29:X:11:ARG:O	29:X:14:ARG:NH2	2.23	0.71
58:h:2351:A:N3	58:h:2396:A:O2'	2.23	0.71
5:7:580:GLU:HG2	5:7:584:ARG:HE	1.55	0.71
34:c:6:ASP:O	34:c:8:ARG:N	2.21	0.71
57:1:63:GLU:N	57:1:63:GLU:OE1	2.24	0.71
58:h:681:C:H2'	58:h:682:A:H8	1.54	0.71
45:o:53:LYS:NZ	58:h:1224:G:O5'	2.23	0.71
5:7:36:LYS:NZ	5:7:95:THR:O	2.22	0.71
14:I:68:ILE:HD13	14:I:99:LEU:HD23	1.73	0.71
58:h:2351:A:H2'	58:h:2352:C:C6	2.26	0.71
50:t:135:GLU:N	50:t:135:GLU:OE1	2.24	0.71
6:A:654:G:H2'	6:A:655:A:H8	1.56	0.70
50:t:110:ASP:OD1	50:t:113:THR:OG1	2.05	0.70
58:h:2345:U:OP1	58:h:2391:G:N2	2.24	0.70
27:V:151:ILE:HA	27:V:154:MET:HB3	1.73	0.70
2:3:8:LYS:NZ	58:h:2253:A:OP2	2.22	0.70
34:c:8:ARG:NH1	58:h:2509:C:OP2	2.23	0.70
57:1:46:ALA:HB2	58:h:571:A:H4'	1.74	0.70
39:i:163:ILE:HD12	39:i:175:LEU:HB3	1.73	0.70
44:n:1:MET:N	44:n:21:VAL:O	2.24	0.70
6:A:722:G:OP2	20:O:35:ARG:NH2	2.25	0.70
8:C:61:ASP:HB2	8:C:96:LYS:HG2	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:G:49:GLN:OE1	12:G:53:LYS:NZ	2.25	0.70
35:d:36:ASN:ND2	58:h:555:G:OP1	2.25	0.70
6:A:1018:C:H2'	6:A:1019:U:H6	1.57	0.70
36:e:43:ARG:NH2	58:h:2587:U:OP2	2.25	0.69
44:n:95:VAL:HG12	44:n:124:ILE:HG21	1.74	0.69
6:A:1266:U:H2'	6:A:1267:U:H5''	1.73	0.69
6:A:408:G:O3'	9:D:104:ARG:NH1	2.24	0.69
8:C:125:ASN:O	8:C:126:ARG:NE	2.20	0.69
58:h:747:A:N6	58:h:768:G:O2'	2.25	0.69
3:4:18:G:O2'	3:4:19:C:OP2	2.11	0.69
42:l:144:MET:SD	42:l:144:MET:N	2.64	0.69
6:A:1338:G:H2'	6:A:1339:A:C8	2.27	0.69
13:H:48:ASP:OD1	13:H:49:TYR:N	2.25	0.69
53:w:51:GLY:HA2	53:w:56:GLU:HG3	1.73	0.69
58:h:1627:U:H2'	58:h:1628:A:H8	1.57	0.69
6:A:1375:G:N2	6:A:1486:A:H8	1.90	0.69
36:e:47:ARG:NH2	58:h:725:A:OP2	2.25	0.69
42:l:24:GLN:HE22	42:l:29:TYR:HB2	1.58	0.69
12:G:79:ARG:HA	12:G:84:THR:HA	1.74	0.69
6:A:427:U:OP1	9:D:13:ARG:NH2	2.26	0.69
21:P:12:LYS:NZ	21:P:15:ASN:OD1	2.25	0.69
6:A:438:U:O2'	6:A:439:U:O2	2.09	0.68
39:i:31:LYS:NZ	58:h:1647:G:N7	2.39	0.68
45:o:28:TYR:OH	58:h:1224:G:O2'	2.11	0.68
58:h:1706:A:H2'	58:h:1707:G:H8	1.55	0.68
6:A:1289:U:OP1	18:M:101:GLN:NE2	2.26	0.68
17:L:114:ARG:HG2	17:L:119:ALA:HB3	1.74	0.68
44:n:9:VAL:HG23	44:n:12:LEU:HB2	1.76	0.68
24:S:55:ARG:HG2	24:S:56:LYS:HE3	1.74	0.68
26:U:68:ARG:HH22	58:h:1449:C:H5''	1.57	0.68
4:5:82:ARG:NE	4:5:88:LEU:O	2.26	0.68
14:I:48:PHE:HE1	14:I:83:ILE:HD11	1.58	0.68
41:k:55:ARG:NH2	58:h:789:G:OP1	2.27	0.68
58:h:2552:A:H2'	58:h:2553:G:C8	2.29	0.68
27:V:135:LEU:HD22	27:V:139:ARG:HH22	1.56	0.68
15:J:45:GLU:OE1	15:J:71:LYS:NZ	2.27	0.68
51:u:57:LYS:O	51:u:62:ASN:ND2	2.26	0.68
5:7:324:VAL:O	5:7:424:GLY:N	2.27	0.68
35:d:28:ARG:NH2	58:h:210:G:OP1	2.25	0.67
6:A:23:C:OP1	10:E:155:SER:OG	2.12	0.67
5:7:677:ASP:OD1	5:7:678:ALA:N	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:o:32:THR:HG22	45:o:34:ALA:H	1.58	0.67
36:e:47:ARG:HH22	58:h:725:A:P	2.17	0.67
6:A:694:G:H2'	6:A:695:A:C8	2.30	0.67
45:o:26:THR:HG22	45:o:105:ILE:HA	1.76	0.67
6:A:1086:G:O2'	8:C:169:ARG:NH1	2.28	0.67
41:k:160:ARG:NH1	58:h:706:G:O2'	2.28	0.67
13:H:13:ARG:HD3	13:H:27:LEU:HD22	1.77	0.67
34:c:40:LYS:NZ	58:h:2571:C:OP1	2.28	0.67
5:7:520:LEU:HD11	5:7:640:LEU:HB3	1.76	0.66
6:A:136:G:O2'	22:Q:7:PRO:O	2.12	0.66
12:G:54:THR:HG1	12:G:56:THR:HG1	1.42	0.66
36:e:23:VAL:HG11	36:e:47:ARG:HD3	1.77	0.66
38:g:16:CYS:SG	38:g:38:CYS:HB3	2.35	0.66
5:7:575:PHE:O	5:7:578:SER:OG	2.14	0.66
49:s:31:LYS:HE3	58:h:658:U:H5'	1.75	0.66
7:B:58:A:O4'	42:l:31:ASN:ND2	2.28	0.66
8:C:62:ARG:NH2	8:C:99:GLN:OE1	2.29	0.66
43:m:140:GLN:NE2	58:h:2969:C:O2	2.28	0.66
58:h:1996:U:OP2	58:h:2001:A:N6	2.25	0.66
6:A:1159:G:N2	6:A:1162:G:OP2	2.29	0.66
6:A:1220:A:H62	6:A:1281:A:H62	1.43	0.66
6:A:1374:U:O2'	6:A:1516:U:OP1	2.12	0.66
9:D:183:ARG:NH1	9:D:183:ARG:O	2.29	0.66
27:V:16:PHE:O	27:V:203:ASN:ND2	2.28	0.66
58:h:993:G:O2'	58:h:994:A:O4'	2.13	0.66
58:h:994:A:N6	58:h:1014:G:O2'	2.29	0.66
58:h:996:G:H2'	58:h:997:G:H8	1.60	0.66
43:m:159:LYS:NZ	58:h:2883:G:OP1	2.28	0.66
58:h:218:A:N3	58:h:234:U:O2'	2.30	0.65
5:7:98:TYR:HD1	5:7:100:ASP:H	1.41	0.65
5:7:229:ILE:HD13	5:7:237:LEU:HB3	1.77	0.65
29:X:25:ARG:NH1	29:X:35:GLU:OE1	2.29	0.65
39:i:66:ASP:OD2	39:i:103:ARG:NH1	2.29	0.65
1:2:27:G:H2'	1:2:28:G:H8	1.61	0.65
6:A:408:G:O2'	9:D:104:ARG:NH2	2.28	0.65
11:F:10:LEU:HB2	11:F:59:ILE:HB	1.78	0.65
6:A:1375:G:H21	6:A:1486:A:H8	1.45	0.65
14:I:38:ARG:HG2	14:I:86:HIS:HB2	1.78	0.65
58:h:2356:G:H2'	58:h:2380:G:H1	1.60	0.65
6:A:943:U:OP2	6:A:1204:C:O2'	2.11	0.65
47:q:114:LEU:O	47:q:118:ILE:HG13	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:h:669:G:O2'	58:h:1369:A:OP1	2.15	0.65
16:K:47:GLN:OE1	16:K:47:GLN:N	2.28	0.65
48:r:34:GLY:N	48:r:37:ASP:OD2	2.29	0.65
5:7:178:PRO:HA	5:7:188:VAL:HA	1.78	0.65
42:l:52:ARG:NH2	42:l:85:LYS:HB2	2.12	0.65
42:l:95:ARG:NH2	58:h:2538:A:OP1	2.28	0.65
47:q:19:ASP:OD1	47:q:21:SER:OG	2.15	0.65
15:J:59:LYS:HE2	15:J:62:ARG:HH21	1.62	0.65
5:7:293:PRO:HA	5:7:296:HIS:HB3	1.79	0.64
41:k:118:ARG:NH1	41:k:191:ALA:O	2.29	0.64
6:A:92:A:O2'	6:A:93:C:O5'	2.14	0.64
27:V:135:LEU:HD22	27:V:139:ARG:NH2	2.12	0.64
27:V:143:LYS:HA	27:V:146:ARG:HE	1.63	0.64
50:t:124:LYS:NZ	58:h:2691:C:O2	2.30	0.64
58:h:1189:G:H1'	58:h:1207:G:H2'	1.79	0.64
6:A:259:G:OP1	25:T:36:ARG:NH2	2.30	0.64
9:D:51:GLN:O	9:D:55:LYS:HG3	1.97	0.64
13:H:103:VAL:HG23	13:H:114:THR:HG23	1.80	0.64
41:k:139:LYS:NZ	58:h:401:C:OP2	2.23	0.64
58:h:1550:G:O6	58:h:1620:U:O4	2.14	0.64
58:h:3014:A:O2'	58:h:3015:C:H5''	1.97	0.64
6:A:823:U:O4	6:A:826:U:N3	2.30	0.64
58:h:2249:G:H2'	58:h:2250:A:C8	2.33	0.64
6:A:146:A:H2'	6:A:147:U:C6	2.32	0.64
6:A:935:G:O6	18:M:104:LYS:NZ	2.30	0.64
47:q:116:ARG:HA	47:q:119:GLN:HG3	1.80	0.64
5:7:24:ARG:N	5:7:89:LYS:O	2.26	0.64
5:7:269:ILE:HG12	5:7:285:ILE:HD13	1.78	0.64
14:I:32:ARG:HD3	14:I:97:GLY:HA3	1.80	0.64
19:N:21:TYR:HE2	19:N:23:ARG:HE	1.46	0.64
46:p:23:ALA:HB3	46:p:24:PRO:HD3	1.80	0.64
58:h:324:C:O2	58:h:452:G:N2	2.31	0.64
5:7:103:GLY:HA3	5:7:474:THR:HG21	1.80	0.64
11:F:94:ASP:OD1	11:F:95:LYS:N	2.28	0.64
27:V:91:TYR:H	27:V:150:GLY:HA3	1.61	0.64
58:h:543:U:H3'	58:h:544:U:H5''	1.79	0.64
5:7:551:VAL:HG22	5:7:604:VAL:HG13	1.80	0.64
6:A:1410:C:H2'	6:A:1411:A:H8	1.63	0.64
6:A:1106:U:O4	15:J:9:ARG:NH1	2.31	0.64
6:A:1330:U:H4'	14:I:142:ARG:HD3	1.78	0.64
20:O:43:LEU:HD13	20:O:53:ARG:HG2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:111:LEU:HD11	27:V:151:ILE:HG22	1.80	0.64
39:i:23:GLU:OE1	39:i:23:GLU:N	2.29	0.64
43:m:169:GLN:OE1	43:m:169:GLN:N	2.31	0.64
6:A:203:U:H2'	6:A:204:A:H8	1.63	0.63
26:U:34:HIS:ND1	26:U:36:ASP:OD1	2.31	0.63
40:j:94:GLU:OE1	40:j:94:GLU:N	2.25	0.63
5:7:346:ILE:HB	5:7:407:VAL:HB	1.80	0.63
58:h:380:A:N3	58:h:401:C:O2'	2.29	0.63
58:h:1710:A:H61	58:h:1716:A:H5''	1.63	0.63
58:h:2358:A:HO2'	58:h:2382:G:HO2'	1.46	0.63
51:u:14:SER:OG	58:h:2913:U:O2'	2.16	0.63
13:H:41:LYS:HZ3	13:H:48:ASP:HA	1.63	0.63
6:A:1418:G:H2'	6:A:1419:C:C6	2.33	0.63
18:M:23:TYR:HE2	18:M:70:LEU:HD22	1.62	0.63
58:h:639:C:HO2'	58:h:640:G:H8	1.46	0.63
15:J:54:SER:O	19:N:41:ARG:NH1	2.31	0.63
58:h:1710:A:N6	58:h:1716:A:OP2	2.31	0.63
6:A:928:A:H2'	6:A:929:G:C8	2.33	0.63
11:F:23:LEU:HD13	11:F:63:ILE:HD11	1.81	0.63
45:o:25:VAL:HG13	45:o:77:THR:HG23	1.80	0.63
27:V:139:ARG:HD3	27:V:139:ARG:N	2.14	0.63
58:h:2862:G:O2'	58:h:3002:A:N6	2.31	0.63
1:2:26:A:H61	1:2:44:G:H1	1.46	0.63
8:C:11:ARG:NH2	8:C:175:LEU:O	2.30	0.63
17:L:86:ARG:HD3	17:L:94:ARG:NH2	2.14	0.63
21:P:60:LEU:HD11	21:P:74:LEU:HD21	1.79	0.63
26:U:19:LYS:NZ	58:h:1455:U:OP1	2.31	0.63
43:m:88:MET:HE1	43:m:146:SER:HB3	1.81	0.63
58:h:1705:C:H2'	58:h:1706:A:H8	1.63	0.63
58:h:2410:A:H2'	58:h:2411:U:C6	2.33	0.63
5:7:81:ALA:HB3	5:7:92:LEU:HB2	1.81	0.62
15:J:26:VAL:O	15:J:30:THR:HG23	1.99	0.62
29:X:64:PRO:HB3	58:h:759:G:H1	1.64	0.62
38:g:15:GLN:OE1	38:g:15:GLN:N	2.32	0.62
35:d:14:ARG:NH2	58:h:885:G:OP2	2.32	0.62
50:t:54:ILE:HG13	50:t:121:ALA:HB2	1.80	0.62
58:h:1704:U:H2'	58:h:1705:C:C6	2.34	0.62
4:5:99:SER:O	4:5:100:ALA:C	2.42	0.62
5:7:677:ASP:CG	5:7:678:ALA:H	2.06	0.62
6:A:693:G:H2'	6:A:694:G:C8	2.34	0.62
6:A:1265:U:H5''	6:A:1266:U:H4'	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:127:GLY:N	10:E:147:ASP:OD2	2.33	0.62
43:m:23:ASN:OD1	43:m:24:LEU:N	2.33	0.62
58:h:1003:A:H1'	58:h:1004:C:H2'	1.80	0.62
45:o:54:ASN:ND2	45:o:73:PHE:O	2.32	0.62
47:q:116:ARG:NH2	58:h:615:A:OP2	2.32	0.62
58:h:2412:U:H2'	58:h:2413:G:C8	2.34	0.62
5:7:304:PRO:HG3	5:7:433:PRO:HG2	1.82	0.62
6:A:39:G:N3	17:L:115:SER:OG	2.32	0.62
12:G:113:GLU:OE1	12:G:122:ASN:ND2	2.32	0.62
58:h:1690:A:H2'	58:h:1691:A:C8	2.34	0.62
5:7:666:ARG:NH1	5:7:691:GLU:O	2.29	0.62
58:h:1544:U:O4	58:h:1626:G:O6	2.18	0.62
58:h:2902:A:H2'	58:h:2903:A:C8	2.34	0.62
6:A:1160:A:OP2	14:I:115:ARG:NH2	2.33	0.62
9:D:74:ALA:HB1	9:D:84:ASN:HB2	1.80	0.62
25:T:55:SER:HB3	25:T:76:LYS:HD3	1.81	0.62
28:W:158:THR:OG1	28:W:174:PRO:O	2.13	0.62
30:Y:36:VAL:HG12	30:Y:63:ARG:HH21	1.64	0.62
39:i:163:ILE:HG22	39:i:178:PRO:HD3	1.81	0.62
42:l:101:ASP:O	42:l:105:GLU:HG2	1.99	0.62
50:t:36:ALA:HB2	50:t:103:LEU:HD11	1.82	0.62
10:E:140:LEU:HD11	10:E:148:ILE:HD13	1.82	0.62
18:M:56:LEU:O	18:M:60:ILE:HG23	2.00	0.62
58:h:681:C:H2'	58:h:682:A:C8	2.34	0.62
58:h:2086:U:H3	58:h:2096:G:H1	1.48	0.62
6:A:380:G:N2	6:A:383:A:OP2	2.26	0.62
9:D:53:LYS:HD3	9:D:198:LEU:HD23	1.80	0.62
10:E:63:ILE:HG12	10:E:139:VAL:HG22	1.82	0.62
10:E:133:GLY:O	10:E:137:ARG:HB3	2.00	0.62
45:o:36:LEU:HD12	58:h:1203:A:H61	1.65	0.62
6:A:986:G:N2	6:A:1016:G:H1	1.98	0.62
11:F:16:GLU:OE1	11:F:16:GLU:N	2.31	0.62
13:H:8:ALA:O	13:H:12:THR:HG22	2.00	0.62
58:h:2364:C:H2'	58:h:2365:A:H8	1.65	0.62
6:A:207:G:H4'	25:T:56:ARG:HG2	1.81	0.61
16:K:27:HIS:NE2	16:K:92:ASP:OD1	2.31	0.61
37:f:25:VAL:HB	37:f:34:GLN:HG3	1.82	0.61
6:A:663:G:N2	16:K:49:ASN:OD1	2.32	0.61
10:E:136:ALA:O	10:E:140:LEU:HB2	2.00	0.61
47:q:68:LYS:NZ	58:h:1258:C:OP2	2.27	0.61
29:X:41:ARG:NH1	58:h:2610:C:O2'	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:h:1613:G:H2'	58:h:1614:G:C8	2.35	0.61
5:7:571:VAL:HG22	5:7:611:ALA:HB2	1.81	0.61
6:A:332:G:O4'	25:T:7:GLN:NE2	2.32	0.61
16:K:103:GLU:OE1	16:K:103:GLU:N	2.33	0.61
27:V:151:ILE:H	27:V:151:ILE:HD12	1.66	0.61
58:h:2470:A:H2'	58:h:2471:A:C8	2.36	0.61
58:h:2482:U:O2'	58:h:2651:C:OP2	2.18	0.61
5:7:394:SER:HB2	5:7:401:GLN:HB3	1.81	0.61
5:7:467:ARG:O	5:7:471:GLU:HG3	2.00	0.61
6:A:926:G:N1	6:A:1320:G:OP2	2.26	0.61
6:A:1158:G:OP2	14:I:119:LYS:NZ	2.33	0.61
58:h:1223:U:H2'	58:h:1224:G:H8	1.64	0.61
6:A:988:C:H2'	6:A:989:G:O4'	2.01	0.61
45:o:53:LYS:HB2	45:o:56:LEU:HB2	1.83	0.61
46:p:55:VAL:HG22	46:p:79:LYS:HD2	1.83	0.61
6:A:146:A:H2'	6:A:147:U:H6	1.66	0.61
14:I:48:PHE:CE1	14:I:83:ILE:HD11	2.36	0.61
15:J:66:GLU:HB3	19:N:59:SER:HB2	1.82	0.61
40:j:111:TYR:CE1	40:j:181:LYS:HG3	2.36	0.61
45:o:51:VAL:HG22	45:o:78:ALA:HA	1.83	0.61
6:A:1328:A:OP1	14:I:142:ARG:NH2	2.25	0.61
8:C:62:ARG:HH22	8:C:64:ARG:HB2	1.66	0.61
13:H:5:ASP:OD1	13:H:79:ARG:NH1	2.34	0.61
58:h:217:G:H22	58:h:235:U:H4'	1.65	0.61
58:h:2106:A:H3'	58:h:2107:G:H5''	1.83	0.61
6:A:208:G:H4'	25:T:59:ASP:HB3	1.83	0.60
6:A:452:A:H62	21:P:93:LEU:HA	1.66	0.60
31:Z:14:THR:N	31:Z:17:GLU:OE1	2.33	0.60
39:i:96:HIS:CE1	39:i:102:LYS:HD3	2.36	0.60
41:k:150:GLU:OE1	41:k:150:GLU:N	2.32	0.60
45:o:6:LYS:O	45:o:10:VAL:HG23	2.01	0.60
39:i:88:ARG:NH2	58:h:2034:G:OP1	2.33	0.60
58:h:2354:G:O2'	58:h:2356:G:N3	2.32	0.60
58:h:2922:U:H2'	58:h:2923:C:C6	2.36	0.60
9:D:105:THR:HG23	9:D:108:MET:H	1.66	0.60
5:7:322:ALA:HB3	5:7:427:LEU:HB2	1.82	0.60
30:Y:39:VAL:HG21	30:Y:64:ALA:HB3	1.83	0.60
58:h:1199:U:H2'	58:h:1200:U:C6	2.35	0.60
4:5:100:ALA:HB1	4:5:102:LYS:NZ	2.16	0.60
5:7:534:HIS:HE1	5:7:536:LYS:HD3	1.65	0.60
52:v:127:PHE:O	58:h:2601:A:O2'	2.18	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:21:U:H2'	6:A:22:C:C6	2.36	0.60
6:A:1477:A:H4'	6:A:1478:G:OP1	2.01	0.60
9:D:85:LEU:O	9:D:89:LEU:HG	2.00	0.60
10:E:39:ARG:HG3	10:E:142:CYS:SG	2.41	0.60
28:W:43:ASP:OD1	28:W:43:ASP:N	2.34	0.60
39:i:230:ASP:OD1	58:h:895:G:N1	2.31	0.60
58:h:327:U:O2	58:h:449:G:N2	2.33	0.60
58:h:2339:G:O6	58:h:2394:A:N6	2.35	0.60
5:7:110:ARG:NH2	5:7:437:ARG:O	2.35	0.60
6:A:187:U:O2	6:A:201:G:O6	2.20	0.60
6:A:819:U:H3	6:A:829:G:H22	1.48	0.60
6:A:936:G:H21	6:A:1208:A:H62	1.49	0.60
52:v:12:GLU:O	52:v:16:ASN:ND2	2.35	0.60
6:A:1184:C:OP1	19:N:2:ALA:N	2.35	0.60
17:L:25:LYS:HD2	17:L:59:SER:HB3	1.84	0.60
24:S:12:ASP:OD1	24:S:12:ASP:N	2.34	0.60
49:s:32:THR:HG22	49:s:35:ARG:H	1.67	0.60
5:7:700:ARG:HD2	5:7:705:GLY:HA2	1.84	0.60
6:A:1298:G:N1	6:A:1301:A:OP2	2.33	0.60
36:e:19:THR:HG23	58:h:745:G:H5''	1.82	0.60
5:7:354:VAL:HB	5:7:386:GLU:HB3	1.82	0.59
6:A:1220:A:H62	6:A:1281:A:N6	1.99	0.59
6:A:1229:A:H4'	14:I:53:ARG:HH12	1.67	0.59
8:C:96:LYS:HG3	8:C:97:GLN:H	1.66	0.59
11:F:30:ILE:HD11	11:F:75:LEU:HD13	1.84	0.59
27:V:219:SER:O	27:V:223:GLU:HG2	2.00	0.59
31:Z:48:ARG:O	31:Z:52:GLN:HG2	2.01	0.59
9:D:93:LEU:HD12	9:D:130:TYR:HB3	1.83	0.59
46:p:132:GLY:HA2	46:p:135:ARG:HD2	1.83	0.59
58:h:1441:C:O2'	58:h:2234:G:O2'	2.21	0.59
5:7:322:ALA:N	5:7:427:LEU:O	2.34	0.59
6:A:1177:A:O2'	6:A:1178:A:OP1	2.21	0.59
10:E:174:ARG:HB2	10:E:177:GLU:HG3	1.83	0.59
58:h:357:U:H4'	58:h:358:G:O5'	2.02	0.59
58:h:470:G:H22	58:h:480:U:H3	1.51	0.59
58:h:3012:U:O2'	58:h:3030:A:N3	2.35	0.59
58:h:928:U:H2'	58:h:929:C:C6	2.38	0.59
58:h:1553:C:H5''	58:h:1554:U:H5	1.67	0.59
58:h:1624:U:HO2'	58:h:1625:G:H8	1.50	0.59
5:7:27:ALA:HA	5:7:93:ILE:HB	1.85	0.59
5:7:371:ALA:HB2	5:7:476:ARG:HD3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:60:U:H2'	6:A:61:G:H8	1.66	0.59
9:D:102:LEU:HD12	9:D:102:LEU:H	1.68	0.59
39:i:85:ASP:OD2	39:i:88:ARG:NH1	2.33	0.59
6:A:275:G:OP1	22:Q:31:LYS:NZ	2.36	0.59
16:K:37:ASN:HA	16:K:67:SER:HB3	1.83	0.59
25:T:53:ALA:O	25:T:57:LYS:HG3	2.03	0.59
33:b:10:ARG:O	33:b:14:ARG:HG3	2.02	0.59
58:h:1627:U:H2'	58:h:1628:A:C8	2.36	0.59
58:h:2338:G:H4'	58:h:2388:G:H22	1.67	0.59
5:7:395:PHE:N	5:7:402:ARG:O	2.35	0.59
18:M:59:TYR:O	18:M:63:ASN:ND2	2.34	0.59
34:c:10:LYS:NZ	58:h:2644:C:OP1	2.36	0.59
46:p:17:ALA:HB1	46:p:48:THR:HB	1.85	0.59
49:s:70:ARG:NH1	58:h:2630:A:C6	2.71	0.59
8:C:32:VAL:O	8:C:36:VAL:HG23	2.02	0.59
10:E:132:ALA:O	10:E:137:ARG:NH1	2.35	0.59
43:m:111:SER:OG	58:h:2891:C:N3	2.33	0.59
58:h:1468:A:H2'	58:h:1469:A:C8	2.37	0.59
6:A:481:G:H2'	6:A:482:A:H8	1.67	0.59
8:C:51:ILE:HD12	8:C:67:ILE:HD11	1.84	0.59
10:E:192:ALA:O	10:E:196:LYS:HG3	2.02	0.59
6:A:708:A:H2'	6:A:709:A:C8	2.37	0.59
9:D:138:ILE:HB	9:D:175:ILE:HB	1.83	0.59
21:P:16:PRO:HB2	21:P:18:TYR:CE1	2.38	0.59
58:h:1937:U:H2'	58:h:1938:G:O4'	2.03	0.59
6:A:928:A:H2'	6:A:929:G:H8	1.68	0.58
58:h:499:G:OP2	58:h:2630:A:O2'	2.19	0.58
58:h:857:U:H2'	58:h:858:A:C8	2.39	0.58
58:h:1186:G:H2'	58:h:1187:A:C5	2.38	0.58
58:h:1613:G:H2'	58:h:1614:G:H8	1.68	0.58
11:F:5:GLU:OE2	23:R:33:LYS:NZ	2.24	0.58
17:L:73:ASN:ND2	17:L:105:GLN:HG3	2.18	0.58
45:o:51:VAL:N	58:h:1202:A:OP1	2.36	0.58
58:h:1208:U:N3	58:h:1220:C:H1'	2.15	0.58
5:7:534:HIS:CE1	5:7:536:LYS:HD3	2.38	0.58
6:A:175:A:H2'	6:A:176:A:H8	1.67	0.58
6:A:826:U:H2'	6:A:828:G:H5'	1.84	0.58
8:C:34:GLU:OE1	8:C:58:ARG:NH1	2.36	0.58
16:K:41:VAL:HG11	16:K:76:ALA:HA	1.85	0.58
58:h:1170:C:H2'	58:h:1171:C:C6	2.37	0.58
6:A:1305:G:H2'	6:A:1306:A:C8	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:191:PRO:HD2	10:E:194:MET:HE3	1.86	0.58
15:J:80:THR:HB	15:J:83:THR:HG23	1.85	0.58
42:l:13:GLN:O	42:l:17:GLU:HG2	2.04	0.58
46:p:114:LYS:O	46:p:118:LEU:CB	2.51	0.58
56:z:18:ARG:NE	58:h:1436:C:O2'	2.37	0.58
5:7:468:LEU:O	5:7:472:ASP:N	2.22	0.58
25:T:52:HIS:O	25:T:56:ARG:HG3	2.04	0.58
30:Y:16:LYS:HD2	30:Y:24:ARG:HB3	1.86	0.58
46:p:49:GLU:HA	46:p:52:ARG:HH21	1.69	0.58
58:h:997:G:H21	58:h:1011:A:H61	1.51	0.58
5:7:338:LEU:HD11	5:7:396:PRO:HG3	1.86	0.58
6:A:335:C:H2'	6:A:336:A:H8	1.69	0.58
6:A:857:U:O2'	13:H:15:ARG:NH1	2.35	0.58
27:V:44:GLN:OE1	27:V:44:GLN:N	2.29	0.58
35:d:38:ARG:HG3	35:d:45:LEU:HD21	1.86	0.58
42:l:87:ARG:H	42:l:90:MET:HE3	1.67	0.58
58:h:2745:C:O2'	58:h:2788:A:N3	2.34	0.58
6:A:642:C:H2'	6:A:643:A:C8	2.39	0.58
21:P:40:TYR:CD2	21:P:73:LEU:HD11	2.39	0.58
45:o:41:ARG:NH2	46:p:119:ASN:HA	2.19	0.58
46:p:114:LYS:HG3	46:p:130:ILE:HD11	1.86	0.58
6:A:32:G:O2'	6:A:296:U:OP1	2.21	0.58
6:A:461:G:O2'	6:A:463:C:N4	2.37	0.58
9:D:99:ARG:HB3	9:D:166:LEU:HD12	1.85	0.58
18:M:5:VAL:HG11	18:M:60:ILE:HD11	1.86	0.58
22:Q:21:LYS:HB2	22:Q:78:GLU:HG3	1.85	0.58
5:7:586:GLN:HB3	5:7:629:LEU:HD23	1.86	0.57
6:A:481:G:H2'	6:A:482:A:C8	2.39	0.57
6:A:654:G:H2'	6:A:655:A:C8	2.37	0.57
6:A:1163:G:H4'	6:A:1164:U:H5'	1.86	0.57
53:w:19:PHE:O	53:w:49:ARG:NH1	2.37	0.57
58:h:680:U:H2'	58:h:681:C:C6	2.39	0.57
6:A:505:C:H2'	6:A:506:C:C6	2.39	0.57
6:A:523:U:OP2	9:D:10:ARG:NH1	2.36	0.57
14:I:41:LEU:HD12	14:I:42:VAL:N	2.19	0.57
45:o:9:ALA:O	45:o:13:ILE:HG13	2.04	0.57
58:h:1002:C:H2'	58:h:1003:A:H5''	1.85	0.57
13:H:115:ASP:N	13:H:115:ASP:OD1	2.37	0.57
27:V:120:MET:HE1	27:V:129:ARG:HH21	1.69	0.57
28:W:109:GLU:OE2	28:W:132:GLU:HB3	2.03	0.57
49:s:15:GLU:OE1	58:h:691:U:O2'	2.12	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:h:2255:A:N3	58:h:2679:G:O2'	2.33	0.57
1:2:38:A:O2'	6:A:770:A:OP1	2.20	0.57
2:3:17:ASN:ND2	58:h:1103:C:O2	2.36	0.57
58:h:1706:A:H2'	58:h:1707:G:C8	2.38	0.57
6:A:690:G:OP1	11:F:54:LYS:NZ	2.35	0.57
6:A:904:G:H2'	6:A:905:A:C8	2.39	0.57
6:A:995:A:OP1	24:S:17:LYS:NZ	2.37	0.57
12:G:65:ALA:O	12:G:69:VAL:HG23	2.05	0.57
45:o:53:LYS:HZ2	58:h:1224:G:C5'	2.18	0.57
58:h:2334:U:O2'	58:h:2341:U:O2'	2.14	0.57
6:A:490:A:HO2'	6:A:522:G:HO2'	1.51	0.57
6:A:986:G:H22	6:A:1016:G:H1	1.50	0.57
38:g:16:CYS:SG	38:g:17:GLY:N	2.78	0.57
58:h:1224:G:H2'	58:h:1225:G:H8	1.70	0.57
1:2:41:C:O2'	6:A:1320:G:N3	2.38	0.57
6:A:1199:C:H2'	6:A:1200:A:C8	2.40	0.57
6:A:1410:C:H2'	6:A:1411:A:C8	2.39	0.57
27:V:135:LEU:HB3	27:V:139:ARG:NH2	2.20	0.57
28:W:39:GLY:HA3	28:W:99:VAL:HB	1.86	0.57
58:h:337:U:H5'	58:h:338:C:H5''	1.87	0.57
58:h:1468:A:H2'	58:h:1469:A:H8	1.68	0.57
5:7:25:ASN:HB2	5:7:113:ASP:H	1.68	0.57
16:K:93:VAL:HG11	16:K:106:ILE:HD11	1.85	0.57
25:T:35:PHE:O	25:T:39:VAL:HG12	2.04	0.57
39:i:108:PRO:HD2	39:i:111:LEU:HD22	1.85	0.57
47:q:27:ARG:NH1	58:h:1130:C:O2	2.38	0.57
58:h:1530:G:H21	58:h:1805:G:H1	1.53	0.57
58:h:2726:G:H5''	58:h:2727:A:H5''	1.86	0.57
9:D:165:TRP:CE2	9:D:181:PRO:HB3	2.40	0.57
58:h:2364:C:H2'	58:h:2365:A:C8	2.39	0.57
2:3:7:LYS:NZ	58:h:1252:G:O4'	2.38	0.57
5:7:110:ARG:HH22	5:7:436:LEU:HB3	1.68	0.57
5:7:450:VAL:HG23	5:7:486:ILE:HG23	1.87	0.57
6:A:872:G:O2'	6:A:888:A:N6	2.38	0.57
10:E:59:THR:HG22	10:E:77:LYS:HB3	1.85	0.56
38:g:35:VAL:HG11	42:l:113:ILE:HD12	1.87	0.56
27:V:187:LEU:HD11	27:V:199:PRO:HB3	1.85	0.56
5:7:301:VAL:HG11	5:7:434:LEU:HD13	1.86	0.56
5:7:523:THR:HG23	5:7:639:ASN:HD22	1.70	0.56
6:A:269:U:H2'	6:A:270:A:H8	1.69	0.56
45:o:87:VAL:O	45:o:91:LYS:HG3	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:q:108:MET:SD	58:h:1256:G:N2	2.64	0.56
58:h:2304:C:H2'	58:h:2305:A:H8	1.70	0.56
5:7:652:PRO:HD2	5:7:655:LEU:HD12	1.86	0.56
6:A:725:A:H2'	6:A:726:G:C8	2.40	0.56
9:D:57:ARG:HH21	9:D:63:MET:HA	1.70	0.56
14:I:49:ASN:HD22	14:I:84:TYR:HD1	1.52	0.56
41:k:118:ARG:NH2	49:s:4:ILE:O	2.38	0.56
58:h:303:G:H2'	58:h:304:U:O4'	2.05	0.56
6:A:725:A:H2'	6:A:726:G:H8	1.70	0.56
6:A:1207:C:H2'	18:M:103:THR:HG22	1.87	0.56
17:L:76:GLU:O	17:L:77:HIS:ND1	2.38	0.56
52:v:73:ILE:HG22	52:v:75:GLY:H	1.71	0.56
6:A:695:A:H2'	6:A:696:A:C8	2.40	0.56
14:I:50:LEU:HD12	14:I:58:TYR:HB3	1.87	0.56
16:K:97:GLY:O	16:K:102:ARG:NH1	2.38	0.56
58:h:334:G:H2'	58:h:335:G:C8	2.41	0.56
58:h:447:A:H2'	58:h:448:U:C6	2.41	0.56
4:5:62:GLU:HG2	4:5:107:LYS:HB2	1.86	0.56
6:A:390:U:H2'	6:A:391:G:C8	2.41	0.56
39:i:83:GLU:OE2	39:i:104:TYR:OH	2.17	0.56
58:h:138:A:H2'	58:h:139:U:O2	2.06	0.56
58:h:3020:U:H1'	58:h:3022:G:O6	2.06	0.56
5:7:15:PRO:HB2	5:7:89:LYS:HE3	1.88	0.56
9:D:11:LYS:HD3	9:D:58:PHE:CD2	2.41	0.56
22:Q:27:VAL:O	22:Q:71:GLY:N	2.37	0.56
37:f:19:ARG:NE	58:h:2980:U:OP2	2.34	0.56
58:h:2019:A:H2'	58:h:2020:A:C8	2.41	0.56
58:h:2387:U:H3'	58:h:2388:G:H8	1.71	0.56
9:D:96:VAL:HG21	9:D:132:VAL:HG11	1.86	0.56
21:P:86:LEU:HB2	21:P:87:PRO:CD	2.36	0.56
44:n:3:LEU:HD13	44:n:36:ALA:HB1	1.88	0.56
45:o:29:ARG:NH1	58:h:1171:C:O2	2.37	0.56
53:w:62:LYS:HE2	53:w:64:SER:HB2	1.86	0.56
58:h:2297:U:H2'	58:h:2298:U:C6	2.41	0.56
6:A:269:U:H2'	6:A:270:A:C8	2.41	0.55
6:A:436:C:H5''	9:D:148:LEU:HD12	1.88	0.55
11:F:40:VAL:HG22	11:F:63:ILE:HG12	1.89	0.55
45:o:110:MET:SD	45:o:111:ASP:N	2.79	0.55
5:7:324:VAL:HG22	5:7:339:VAL:HG22	1.88	0.55
9:D:190:LEU:HD12	9:D:191:THR:H	1.71	0.55
7:B:10:G:O2'	7:B:11:U:OP1	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:D:108:MET:HA	9:D:108:MET:HE2	1.88	0.55
15:J:24:LYS:NZ	15:J:90:ILE:HG23	2.22	0.55
15:J:86:ALA:O	15:J:90:ILE:HG13	2.06	0.55
24:S:41:ILE:HG22	24:S:43:ASP:H	1.71	0.55
6:A:392:C:H5'	21:P:13:ILE:HD11	1.88	0.55
6:A:416:G:H2'	6:A:417:G:H8	1.71	0.55
43:m:158:TYR:O	43:m:172:ARG:NH2	2.33	0.55
6:A:500:A:H62	6:A:509:G:H8	1.53	0.55
6:A:1203:G:OP2	6:A:1304:C:N4	2.37	0.55
15:J:11:LYS:HD3	15:J:71:LYS:HG2	1.88	0.55
52:v:64:SER:OG	52:v:65:SER:N	2.40	0.55
58:h:551:G:N2	58:h:554:A:OP2	2.36	0.55
58:h:756:A:H3'	58:h:757:G:H21	1.72	0.55
5:7:292:ALA:O	5:7:296:HIS:N	2.38	0.55
6:A:449:C:O2	21:P:43:LYS:NZ	2.34	0.55
6:A:1051:C:H2'	6:A:1052:G:H8	1.72	0.55
6:A:1248:U:O2'	6:A:1249:G:O5'	2.25	0.55
27:V:72:THR:O	27:V:77:GLN:NE2	2.38	0.55
58:h:1537:U:H2'	58:h:1538:G:H8	1.71	0.55
5:7:23:ILE:HD13	5:7:411:ASP:HB2	1.89	0.55
6:A:1028:G:OP1	19:N:4:LYS:N	2.28	0.55
7:B:48:C:OP2	52:v:14:ARG:NH1	2.39	0.55
22:Q:39:GLU:OE1	22:Q:39:GLU:N	2.40	0.55
39:i:143:HIS:ND1	39:i:194:GLY:O	2.22	0.55
49:s:63:LYS:HD2	58:h:2618:C:H5''	1.88	0.55
58:h:1174:G:H4'	58:h:1204:A:H8	1.71	0.55
58:h:2329:G:H1	58:h:2406:U:H3	1.53	0.55
6:A:39:G:H2'	6:A:40:C:C6	2.42	0.55
42:l:80:SER:OG	42:l:87:ARG:HA	2.07	0.55
5:7:531:HIS:ND1	5:7:548:ASP:OD2	2.40	0.55
6:A:900:A:H2'	6:A:901:A:C8	2.42	0.55
6:A:1011:U:H1'	6:A:1013:G:H1	1.72	0.55
6:A:1374:U:H2'	6:A:1375:G:C8	2.42	0.55
20:O:78:TYR:O	20:O:82:ILE:HG23	2.06	0.55
40:j:6:ILE:CD1	40:j:31:ALA:HB1	2.36	0.55
42:l:168:THR:OG1	52:v:3:HIS:NE2	2.40	0.55
5:7:186:LYS:O	5:7:199:TYR:N	2.40	0.55
6:A:144:G:H2'	6:A:145:G:C8	2.41	0.55
6:A:593:C:H2'	6:A:594:A:H8	1.72	0.55
9:D:126:ASP:OD1	9:D:126:ASP:N	2.39	0.55
17:L:31:ARG:O	17:L:58:THR:OG1	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:S:36:ARG:HD3	24:S:52:HIS:O	2.06	0.55
38:g:3:THR:OG1	38:g:4:GLY:N	2.39	0.55
46:p:33:HIS:O	46:p:66:ARG:NH2	2.39	0.55
58:h:1007:G:O2'	58:h:1008:G:O5'	2.19	0.55
58:h:1204:A:H4'	58:h:1205:G:N7	2.22	0.55
58:h:2288:C:H2'	58:h:2289:C:H6	1.72	0.55
5:7:320:LEU:HA	5:7:344:GLY:HA3	1.88	0.54
5:7:675:LYS:HE3	46:p:27:GLY:C	2.31	0.54
6:A:1476:A:H5''	17:L:44:LYS:NZ	2.22	0.54
29:X:14:ARG:NH1	58:h:2503:G:N7	2.55	0.54
58:h:1229:A:H8	58:h:1230:G:H1'	1.72	0.54
5:7:394:SER:HA	5:7:403:PRO:HA	1.89	0.54
5:7:458:GLU:HG2	17:L:77:HIS:CD2	2.41	0.54
6:A:956:A:OP1	19:N:29:ARG:NH2	2.39	0.54
11:F:30:ILE:HD13	11:F:65:VAL:HG11	1.88	0.54
32:a:11:SER:OG	32:a:12:THR:N	2.40	0.54
44:n:114:LYS:NZ	58:h:282:A:OP1	2.40	0.54
58:h:1675:U:O2'	58:h:1676:G:N7	2.40	0.54
5:7:24:ARG:NH2	5:7:287:SER:O	2.37	0.54
5:7:37:THR:OG1	60:7:801:GNP:O1B	2.22	0.54
6:A:1478:G:HO2'	58:h:2136:A:HO2'	1.55	0.54
17:L:46:ASN:HD22	17:L:89:ASP:CG	2.14	0.54
46:p:110:ILE:O	46:p:114:LYS:HG2	2.06	0.54
47:q:102:GLU:OE2	58:h:3004:C:N4	2.39	0.54
1:2:27:G:H2'	1:2:28:G:C8	2.42	0.54
9:D:24:GLN:N	9:D:24:GLN:OE1	2.41	0.54
22:Q:39:GLU:HB3	22:Q:56:THR:HG23	1.89	0.54
27:V:135:LEU:HB3	27:V:139:ARG:HH21	1.73	0.54
58:h:1223:U:H2'	58:h:1224:G:C8	2.42	0.54
58:h:2261:U:H2'	58:h:2262:C:C6	2.43	0.54
6:A:203:U:H2'	6:A:204:A:C8	2.42	0.54
18:M:52:GLN:O	18:M:55:VAL:HG22	2.07	0.54
26:U:10:ILE:HD11	26:U:37:SER:HB3	1.88	0.54
38:g:25:ARG:O	42:l:109:ARG:NH1	2.41	0.54
5:7:257:GLU:HG2	5:7:289:GLY:HA2	1.89	0.54
6:A:1350:U:OP2	14:I:134:LYS:NZ	2.36	0.54
31:Z:34:PHE:O	31:Z:38:THR:HG23	2.08	0.54
58:h:978:A:H2'	58:h:979:G:C8	2.42	0.54
5:7:282:LEU:HA	5:7:285:ILE:HD12	1.88	0.54
5:7:644:VAL:HA	5:7:688:PRO:HA	1.90	0.54
6:A:1202:G:O3'	24:S:77:THR:HG21	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:I:31:ARG:HG2	14:I:36:VAL:HG12	1.89	0.54
27:V:79:SER:O	27:V:83:GLU:HG2	2.07	0.54
33:b:45:LYS:NZ	58:h:3104:A:P	2.81	0.54
41:k:141:ALA:HB1	41:k:169:VAL:HG12	1.89	0.54
46:p:103:THR:O	46:p:107:VAL:HG23	2.07	0.54
6:A:403:C:H5''	9:D:128:PRO:HD2	1.89	0.54
16:K:85:GLU:OE1	16:K:86:HIS:ND1	2.23	0.54
27:V:187:LEU:HD21	27:V:196:VAL:HG21	1.90	0.54
58:h:1476:G:H2'	58:h:1477:C:C6	2.43	0.54
58:h:3023:G:H2'	58:h:3024:A:O4'	2.08	0.54
15:J:59:LYS:HE2	15:J:62:ARG:NH2	2.22	0.54
27:V:166:THR:HG23	27:V:173:VAL:HG11	1.90	0.54
28:W:165:PRO:HD2	28:W:168:VAL:HG21	1.90	0.54
5:7:309:ARG:NE	5:7:310:LYS:O	2.40	0.54
6:A:1018:C:H2'	6:A:1019:U:C6	2.39	0.54
13:H:15:ARG:NH2	13:H:77:LEU:O	2.35	0.54
41:k:143:THR:O	41:k:147:THR:HG23	2.08	0.54
55:y:12:LYS:NZ	58:h:1112:C:O2	2.40	0.54
58:h:196:A:H62	58:h:2654:A:H2'	1.73	0.54
6:A:21:U:H2'	6:A:22:C:H6	1.72	0.53
6:A:716:U:H2'	6:A:717:C:C6	2.43	0.53
7:B:116:C:H2'	7:B:117:A:C8	2.43	0.53
8:C:76:ILE:HG22	8:C:83:ALA:HB2	1.89	0.53
9:D:4:TYR:CZ	9:D:11:LYS:HE2	2.43	0.53
9:D:55:LYS:HB2	9:D:190:LEU:HD22	1.90	0.53
16:K:28:GLY:HA2	16:K:46:PRO:HD3	1.88	0.53
6:A:1098:U:H2'	6:A:1099:C:H6	1.73	0.53
26:U:43:LYS:NZ	58:h:1815:G:OP2	2.38	0.53
42:l:141:GLU:HG3	42:l:143:SER:H	1.73	0.53
58:h:2294:A:H2'	58:h:2295:C:C6	2.43	0.53
5:7:272:CYS:HB2	5:7:277:VAL:HB	1.90	0.53
6:A:122:G:OP1	6:A:585:U:O2'	2.22	0.53
6:A:193:C:N4	22:Q:18:GLY:O	2.39	0.53
27:V:140:GLU:O	27:V:144:LEU:HG	2.08	0.53
40:j:88:ASP:OD1	40:j:88:ASP:N	2.41	0.53
58:h:1177:G:H3'	58:h:1178:U:H2'	1.89	0.53
58:h:2178:G:O2'	58:h:2180:U:O4	2.24	0.53
58:h:2374:U:H2'	58:h:2375:G:C8	2.43	0.53
6:A:1013:G:H2'	6:A:1014:U:O4'	2.08	0.53
8:C:96:LYS:HG3	8:C:97:GLN:N	2.22	0.53
47:q:60:ASP:OD1	47:q:60:ASP:N	2.32	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:h:287:A:N6	58:h:299:G:O2'	2.42	0.53
58:h:1729:A:H2'	58:h:1731:A:C8	2.44	0.53
6:A:87:G:H2'	6:A:88:G:H8	1.73	0.53
6:A:335:C:H2'	6:A:336:A:C8	2.44	0.53
6:A:1019:U:C2	6:A:1020:G:C8	2.96	0.53
6:A:1457:G:H2'	6:A:1458:G:C8	2.43	0.53
8:C:133:MET:HE2	8:C:153:CYS:SG	2.47	0.53
17:L:4:ILE:O	17:L:8:VAL:HG13	2.08	0.53
22:Q:75:SER:O	22:Q:76:LEU:HD23	2.08	0.53
58:h:2288:C:H2'	58:h:2289:C:C6	2.43	0.53
9:D:165:TRP:NE1	9:D:181:PRO:HB3	2.23	0.53
40:j:63:ILE:HD11	58:h:3032:G:H5''	1.89	0.53
49:s:97:GLU:O	49:s:101:LYS:HG2	2.08	0.53
6:A:433:C:H2'	6:A:434:C:C6	2.43	0.53
6:A:1296:C:H2'	6:A:1297:U:C6	2.44	0.53
43:m:102:GLN:H	43:m:102:GLN:CD	2.16	0.53
47:q:49:ASP:HB3	47:q:114:LEU:HD11	1.90	0.53
58:h:1556:A:H2	58:h:1615:G:H1	1.57	0.53
12:G:51:ARG:HE	12:G:58:PRO:HD3	1.74	0.53
27:V:69:PHE:HB3	27:V:80:ILE:HG23	1.91	0.53
27:V:73:LYS:O	27:V:77:GLN:HG3	2.09	0.53
58:h:2224:C:O2'	58:h:2913:U:OP2	2.27	0.53
58:h:2538:A:H2'	58:h:2539:G:H8	1.73	0.53
5:7:196:TYR:N	5:7:207:ARG:O	2.41	0.53
11:F:26:PHE:O	11:F:29:VAL:HG12	2.08	0.53
58:h:1548:C:N4	58:h:1549:G:O6	2.42	0.53
58:h:2515:U:H2'	58:h:2516:U:C6	2.44	0.53
6:A:955:G:OP1	15:J:59:LYS:NZ	2.29	0.53
9:D:140:VAL:HG21	9:D:145:LEU:HD13	1.91	0.53
10:E:176:GLU:OE1	10:E:176:GLU:N	2.33	0.53
12:G:113:GLU:OE2	12:G:118:GLU:HB3	2.09	0.53
22:Q:83:SER:O	22:Q:87:ARG:NH1	2.41	0.53
6:A:485:G:H2'	6:A:486:G:C8	2.43	0.52
14:I:72:LEU:HD23	14:I:107:LEU:HD11	1.90	0.52
15:J:56:HIS:O	15:J:57:LYS:HG2	2.08	0.52
58:h:1211:G:N2	58:h:1216:A:H62	1.97	0.52
14:I:64:HIS:O	14:I:68:ILE:HG13	2.09	0.52
15:J:80:THR:HG22	15:J:82:LYS:H	1.73	0.52
58:h:279:U:H2'	58:h:280:G:H8	1.72	0.52
58:h:1710:A:N6	58:h:1716:A:H5''	2.23	0.52
58:h:2936:C:OP1	58:h:2938:G:H4'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:26:LYS:NZ	27:V:194:ASP:OD2	2.40	0.52
45:o:53:LYS:O	45:o:57:VAL:HG23	2.10	0.52
46:p:94:PRO:HD2	58:h:1194:C:H1'	1.92	0.52
58:h:1704:U:H2'	58:h:1705:C:H6	1.74	0.52
6:A:544:C:C6	22:Q:48:LEU:HD21	2.45	0.52
6:A:927:G:C2	6:A:928:A:C8	2.97	0.52
54:x:120:ASP:OD1	54:x:123:ALA:N	2.41	0.52
58:h:2902:A:H2'	58:h:2903:A:H8	1.73	0.52
6:A:416:G:H2'	6:A:417:G:C8	2.44	0.52
6:A:505:C:P	17:L:88:LYS:HZ1	2.28	0.52
6:A:1014:U:H2'	6:A:1015:G:C8	2.34	0.52
9:D:120:VAL:HG22	9:D:138:ILE:HG12	1.90	0.52
11:F:52:ILE:HD12	11:F:87:ARG:CZ	2.40	0.52
25:T:45:ASP:N	25:T:45:ASP:OD1	2.42	0.52
27:V:30:PHE:HD2	27:V:201:PRO:HG3	1.74	0.52
52:v:31:GLY:N	52:v:54:ASP:OD2	2.37	0.52
55:y:39:VAL:HG11	55:y:42:VAL:HG23	1.92	0.52
58:h:1193:C:H2'	58:h:1194:C:C6	2.44	0.52
5:7:127:GLU:HA	5:7:130:LYS:HD2	1.90	0.52
6:A:81:C:H3'	6:A:82:U:H5''	1.91	0.52
6:A:103:G:N7	25:T:10:ARG:NH2	2.57	0.52
6:A:863:G:OP2	17:L:6:GLN:NE2	2.40	0.52
7:B:10:G:O2'	7:B:11:U:H5'	2.10	0.52
27:V:12:SER:HA	27:V:208:ARG:HH21	1.75	0.52
29:X:41:ARG:HG3	58:h:2553:G:H21	1.72	0.52
58:h:1011:A:C6	58:h:1012:C:H1'	2.44	0.52
6:A:436:C:O2'	9:D:149:PRO:HG3	2.09	0.52
6:A:522:G:H5''	9:D:10:ARG:HH22	1.75	0.52
18:M:90:LEU:O	18:M:94:ARG:HG2	2.10	0.52
27:V:54:TYR:CE1	27:V:220:ALA:HB2	2.45	0.52
29:X:56:ASP:OD1	29:X:58:THR:HG23	2.09	0.52
40:j:161:PHE:CD1	47:q:81:PRO:HG3	2.45	0.52
50:t:80:GLU:OE2	58:h:2717:U:O2'	2.23	0.52
58:h:277:U:H2'	58:h:278:A:C8	2.45	0.52
58:h:2367:G:H2'	58:h:2369:C:H5'	1.91	0.52
58:h:3022:G:H2'	58:h:3023:G:O4'	2.10	0.52
5:7:213:HIS:HB3	5:7:216:ALA:HB3	1.91	0.52
5:7:553:PRO:HA	5:7:602:ILE:HG22	1.91	0.52
6:A:191:C:H2'	6:A:192:G:O4'	2.09	0.52
6:A:498:C:H2'	6:A:510:G:C8	2.45	0.52
6:A:1153:U:H2'	6:A:1154:C:C6	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:D:43:GLU:OE1	9:D:47:ARG:NH2	2.42	0.52
26:U:47:GLU:HG3	26:U:54:VAL:HG12	1.91	0.52
50:t:71:ASP:OD1	50:t:71:ASP:N	2.33	0.52
58:h:3078:G:N2	58:h:3081:A:OP2	2.26	0.52
1:2:18:G:O2'	1:2:57:G:N2	2.36	0.52
5:7:241:TYR:CD1	5:7:247:ILE:HG12	2.45	0.52
9:D:182:GLU:O	9:D:185:GLN:N	2.40	0.52
42:l:8:LEU:HD12	42:l:9:PRO:HD2	1.92	0.52
51:u:24:LEU:HB3	51:u:44:LEU:HD22	1.91	0.52
58:h:2961:G:H2'	58:h:2962:A:C8	2.45	0.52
5:7:592:THR:OG1	5:7:596:GLY:HA2	2.10	0.52
6:A:737:U:O2'	6:A:861:C:O2	2.27	0.52
6:A:1042:U:H2'	6:A:1043:C:C6	2.45	0.52
20:O:18:HIS:CE1	20:O:21:ASP:HB3	2.44	0.52
57:1:75:ASP:OD2	57:1:101:ASN:HB2	2.10	0.52
58:h:1550:G:O6	58:h:1620:U:C4	2.63	0.52
58:h:2470:A:H2'	58:h:2471:A:H8	1.75	0.52
5:7:458:GLU:HA	5:7:461:LEU:HB2	1.92	0.51
6:A:1199:C:H2'	6:A:1200:A:H8	1.76	0.51
6:A:1232:A:N3	6:A:1352:C:O2'	2.42	0.51
9:D:74:ALA:HB3	9:D:85:LEU:HD22	1.91	0.51
20:O:88:ARG:NH1	58:h:831:A:OP2	2.42	0.51
33:b:45:LYS:HZ1	58:h:3104:A:P	2.33	0.51
39:i:212:MET:HG3	58:h:2008:A:H5''	1.92	0.51
39:i:218:ARG:NH2	58:h:896:A:OP1	2.41	0.51
58:h:667:A:OP2	58:h:2723:C:O2'	2.28	0.51
5:7:475:LEU:HD13	5:7:499:VAL:HG21	1.90	0.51
7:B:15:U:OP2	7:B:71:C:O2'	2.28	0.51
9:D:52:GLU:HG3	9:D:194:LEU:HD12	1.92	0.51
9:D:190:LEU:HD12	9:D:191:THR:N	2.24	0.51
40:j:148:PRO:O	58:h:2735:U:O2'	2.23	0.51
47:q:102:GLU:O	47:q:106:ILE:HG12	2.10	0.51
5:7:579:VAL:HG22	5:7:621:PHE:HB3	1.91	0.51
6:A:638:A:O4'	20:O:22:THR:HG21	2.10	0.51
6:A:653:G:H2'	6:A:654:G:H8	1.75	0.51
6:A:672:U:O2'	6:A:674:G:N7	2.30	0.51
8:C:6:ASN:OD1	8:C:9:GLY:N	2.32	0.51
19:N:47:MET:HG2	19:N:52:GLU:OE1	2.09	0.51
27:V:63:HIS:ND1	27:V:63:HIS:O	2.43	0.51
48:r:13:ASN:OD1	48:r:97:ARG:HG2	2.11	0.51
58:h:1540:U:H3	58:h:1632:G:H1	1.57	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:11:U:O2'	7:B:12:C:H5'	2.11	0.51
39:i:20:ASP:O	39:i:22:ALA:N	2.44	0.51
58:h:1435:C:C5	58:h:1444:U:H5''	2.45	0.51
24:S:18:LYS:O	24:S:22:GLN:HG3	2.09	0.51
25:T:20:ARG:HH22	25:T:64:LYS:HB3	1.75	0.51
28:W:119:THR:OG1	28:W:152:GLU:OE2	2.28	0.51
58:h:1087:G:H2'	58:h:1088:U:C6	2.46	0.51
5:7:44:LEU:HB3	5:7:49:VAL:HB	1.93	0.51
6:A:356:A:N3	6:A:368:U:O2'	2.37	0.51
6:A:485:G:H2'	6:A:486:G:H8	1.76	0.51
6:A:1395:C:H2'	6:A:1396:A:C8	2.45	0.51
37:f:33:LYS:NZ	58:h:2967:C:OP1	2.44	0.51
43:m:106:PHE:HB2	43:m:114:VAL:HG13	1.91	0.51
58:h:297:G:H2'	58:h:298:G:C8	2.46	0.51
58:h:621:U:H2'	58:h:622:C:C6	2.45	0.51
58:h:1696:G:O2'	58:h:1736:G:O6	2.28	0.51
5:7:353:HIS:CD2	5:7:355:SER:HB2	2.46	0.51
34:c:30:ARG:HH11	34:c:30:ARG:HG3	1.74	0.51
42:l:15:TYR:HA	42:l:19:ILE:HG13	1.92	0.51
58:h:389:G:N1	58:h:392:A:OP2	2.38	0.51
58:h:2538:A:H2'	58:h:2539:G:C8	2.46	0.51
5:7:366:GLY:HA3	5:7:370:ALA:HA	1.91	0.51
6:A:1036:U:H5'	8:C:163:SER:OG	2.10	0.51
14:I:75:VAL:HG13	14:I:77:ARG:H	1.76	0.51
42:l:111:ILE:HD11	42:l:181:GLY:C	2.35	0.51
58:h:2383:U:C4	58:h:2384:C:H1'	2.46	0.51
6:A:737:U:H2'	6:A:738:G:O4'	2.10	0.51
6:A:1007:U:O2'	6:A:1008:C:O5'	2.29	0.51
12:G:26:LEU:HD13	12:G:101:LEU:HD22	1.93	0.51
42:l:172:GLU:H	42:l:172:GLU:CD	2.19	0.51
47:q:102:GLU:HG2	47:q:124:VAL:HG11	1.93	0.51
58:h:705:C:H2'	58:h:706:G:H5''	1.93	0.51
5:7:20:PRO:HB2	5:7:294:PRO:HD3	1.93	0.51
6:A:411:A:N6	6:A:413:G:H21	2.08	0.51
6:A:800:U:H4'	6:A:801:G:OP2	2.11	0.51
43:m:87:LYS:HG3	43:m:166:GLU:HB2	1.93	0.51
43:m:161:LYS:NZ	58:h:2881:A:O2'	2.44	0.51
46:p:54:ASN:HB3	46:p:79:LYS:HD3	1.93	0.51
50:t:1:MET:N	50:t:48:GLU:OE1	2.44	0.51
56:z:32:ARG:NH1	56:z:81:VAL:O	2.44	0.51
58:h:2074:G:N2	58:h:2110:U:O4	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:7:296:HIS:ND1	5:7:298:LEU:HD23	2.27	0.50
13:H:114:THR:HG22	13:H:116:ARG:H	1.75	0.50
35:d:21:PHE:HB2	35:d:46:THR:HG21	1.93	0.50
42:l:134:ASN:OD1	42:l:164:VAL:HG13	2.11	0.50
57:1:82:ARG:NH2	58:h:382:A:OP2	2.44	0.50
58:h:277:U:H2'	58:h:278:A:H8	1.76	0.50
58:h:1673:A:H5''	58:h:1674:G:H5''	1.92	0.50
1:2:16:U:O3'	1:2:17:C:H2'	2.11	0.50
6:A:534:U:H2'	6:A:535:C:C6	2.46	0.50
6:A:1486:A:H2	6:A:1489:G:N1	2.07	0.50
38:g:1:MET:HE2	38:g:1:MET:HA	1.94	0.50
46:p:39:GLU:O	46:p:42:LYS:HG3	2.10	0.50
48:r:9:LYS:HB2	48:r:9:LYS:NZ	2.25	0.50
54:x:22:LYS:NZ	58:h:17:C:OP1	2.40	0.50
58:h:998:G:H2'	58:h:999:C:C6	2.46	0.50
58:h:2044:U:H5'	58:h:2195:U:H5'	1.93	0.50
58:h:2327:C:H2'	58:h:2328:G:H8	1.75	0.50
6:A:1060:A:H4'	10:E:46:VAL:HG21	1.91	0.50
21:P:51:ILE:HG21	21:P:77:THR:HG21	1.93	0.50
42:l:41:VAL:HG13	42:l:98:LEU:HB2	1.92	0.50
44:n:62:ILE:H	44:n:65:ALA:HB3	1.76	0.50
58:h:2515:U:OP1	58:h:2604:U:O2'	2.29	0.50
5:7:321:LEU:HB3	5:7:343:SER:HB3	1.94	0.50
5:7:376:GLY:O	5:7:379:HIS:N	2.38	0.50
60:7:801:GNP:H8	60:7:801:GNP:O5'	2.11	0.50
6:A:1329:G:O6	14:I:32:ARG:NH2	2.43	0.50
58:h:49:A:H2'	58:h:50:A:C8	2.47	0.50
58:h:1165:G:N3	58:h:1228:A:C6	2.80	0.50
58:h:2443:U:H2'	58:h:2444:C:H6	1.76	0.50
5:7:565:LYS:N	5:7:606:LEU:O	2.35	0.50
6:A:746:A:OP2	6:A:792:G:N2	2.45	0.50
6:A:1447:C:H2'	6:A:1448:G:H8	1.77	0.50
8:C:105:VAL:HG21	8:C:114:LEU:HD11	1.93	0.50
40:j:173:ASP:OD1	40:j:173:ASP:N	2.42	0.50
58:h:1690:A:H2'	58:h:1691:A:H8	1.76	0.50
58:h:2815:C:H2'	58:h:2816:G:H8	1.76	0.50
4:5:96:LEU:HA	4:5:100:ALA:HB3	1.94	0.50
6:A:987:A:H2'	6:A:988:C:C6	2.46	0.50
6:A:1076:C:H2'	6:A:1077:C:C6	2.46	0.50
47:q:13:ARG:NH1	47:q:121:LYS:HE2	2.27	0.50
48:r:68:GLU:HG2	48:r:78:LYS:HD2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:60:U:H2'	6:A:61:G:C8	2.45	0.50
58:h:1640:A:O2'	58:h:1641:U:OP1	2.27	0.50
6:A:299:G:H2'	6:A:300:A:C8	2.47	0.50
10:E:185:PRO:HG2	10:E:188:ASP:OD2	2.12	0.50
29:X:15:ASP:OD1	29:X:16:SER:N	2.45	0.50
45:o:26:THR:HA	45:o:106:LYS:H	1.77	0.50
58:h:300:G:O2'	58:h:302:U:O4'	2.27	0.50
58:h:1002:C:H2'	58:h:1003:A:H3'	1.93	0.50
58:h:1284:A:H2'	58:h:1285:G:H8	1.77	0.50
58:h:1703:G:H2'	58:h:1704:U:C6	2.46	0.50
5:7:322:ALA:HA	5:7:341:VAL:HA	1.93	0.50
5:7:465:LEU:HA	5:7:468:LEU:HD12	1.94	0.50
6:A:363:A:N7	17:L:27:SER:OG	2.40	0.50
6:A:698:A:H5'	16:K:128:ASN:HB2	1.94	0.50
6:A:1337:A:H2'	6:A:1338:G:H8	1.77	0.50
8:C:129:PHE:O	8:C:133:MET:HG3	2.11	0.50
15:J:53:ARG:NH1	15:J:63:GLU:HB2	2.27	0.50
44:n:5:LEU:HD13	44:n:9:VAL:HG22	1.94	0.50
50:t:65:TRP:HB2	50:t:105:GLU:HB2	1.94	0.50
58:h:672:C:H2'	58:h:673:C:C6	2.47	0.50
58:h:1343:G:H2'	58:h:1345:G:C8	2.46	0.50
58:h:1790:A:H2'	58:h:1791:A:C8	2.47	0.50
5:7:151:ASP:HA	5:7:183:GLU:O	2.11	0.49
5:7:172:VAL:HG22	5:7:266:PHE:HB2	1.93	0.49
5:7:455:LYS:HD3	17:L:33:VAL:HG13	1.94	0.49
6:A:986:G:N1	6:A:1016:G:O6	2.45	0.49
12:G:75:VAL:HG21	12:G:144:MET:HG2	1.94	0.49
13:H:79:ARG:NH2	13:H:81:SER:O	2.45	0.49
24:S:28:LYS:N	24:S:28:LYS:HD3	2.27	0.49
39:i:99:ASP:C	39:i:99:ASP:OD1	2.55	0.49
52:v:18:ARG:NH1	52:v:105:GLY:O	2.45	0.49
58:h:1396:G:H2'	58:h:1397:U:C6	2.47	0.49
58:h:1515:C:H2'	58:h:1516:G:H8	1.76	0.49
58:h:1614:G:H2'	58:h:1615:G:H8	1.76	0.49
58:h:2106:A:OP2	58:h:2106:A:H8	1.96	0.49
58:h:2321:U:H2'	58:h:2322:C:C6	2.47	0.49
5:7:81:ALA:O	5:7:92:LEU:N	2.36	0.49
6:A:846:A:H2'	6:A:847:A:C8	2.47	0.49
6:A:958:G:OP2	6:A:1340:U:O2'	2.29	0.49
6:A:1497:A:H2'	6:A:1498:C:C6	2.48	0.49
27:V:136:MET:HE2	27:V:136:MET:HA	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:l:100:GLY:N	42:l:103:MET:HE2	2.27	0.49
44:n:105:LYS:NZ	44:n:111:ASN:OD1	2.40	0.49
44:n:124:ILE:HG22	44:n:125:LYS:N	2.26	0.49
58:h:742:G:O2'	58:h:2575:G:OP1	2.26	0.49
58:h:795:G:H2'	58:h:796:A:C8	2.47	0.49
58:h:858:A:O2'	58:h:1877:U:OP1	2.26	0.49
5:7:423:THR:OG1	5:7:470:ALA:O	2.20	0.49
8:C:62:ARG:NH2	8:C:99:GLN:HB3	2.28	0.49
9:D:90:GLU:O	9:D:95:ASN:ND2	2.45	0.49
10:E:132:ALA:HB2	10:E:150:ALA:HB3	1.94	0.49
47:q:37:ARG:NH1	58:h:1125:C:OP1	2.45	0.49
58:h:1343:G:H2'	58:h:1345:G:N7	2.27	0.49
5:7:550:GLU:O	5:7:605:THR:N	2.45	0.49
6:A:811:U:H5'	27:V:21:ARG:HG2	1.95	0.49
6:A:1133:G:H4'	15:J:15:HIS:NE2	2.26	0.49
11:F:28:ASN:HA	11:F:31:ARG:HG2	1.95	0.49
17:L:34:CYS:HA	17:L:55:VAL:HA	1.94	0.49
46:p:28:PRO:HG2	58:h:1213:A:H61	1.78	0.49
5:7:527:LYS:HD2	5:7:550:GLU:HG2	1.94	0.49
6:A:185:G:C6	6:A:204:A:C6	3.00	0.49
8:C:68:HIS:HB3	8:C:105:VAL:HG13	1.93	0.49
13:H:70:ARG:HG3	13:H:70:ARG:O	2.13	0.49
14:I:66:GLN:HA	14:I:66:GLN:OE1	2.13	0.49
58:h:89:A:O2'	58:h:90:C:OP1	2.30	0.49
58:h:263:G:H2'	58:h:264:G:O4'	2.13	0.49
58:h:978:A:H2'	58:h:979:G:H8	1.77	0.49
58:h:995:U:H2'	58:h:996:G:C8	2.47	0.49
58:h:2757:C:OP1	58:h:2889:A:O2'	2.28	0.49
58:h:2778:U:H2'	58:h:2779:U:C6	2.47	0.49
58:h:2851:G:N2	58:h:3001:G:OP2	2.45	0.49
6:A:352:C:O2'	6:A:354:G:OP1	2.25	0.49
6:A:1425:G:H5'	6:A:1426:C:C5	2.41	0.49
8:C:36:VAL:HG11	19:N:26:LYS:HG3	1.95	0.49
21:P:73:LEU:O	21:P:77:THR:HG22	2.12	0.49
50:t:58:ILE:HD11	50:t:108:TYR:CG	2.48	0.49
53:w:1:MET:HE1	53:w:3:THR:HA	1.93	0.49
5:7:674:ASP:O	5:7:682:VAL:N	2.34	0.49
6:A:422:C:H4'	6:A:423:G:O5'	2.11	0.49
6:A:1281:A:H2'	6:A:1281:A:N3	2.27	0.49
6:A:1411:A:H2'	6:A:1412:C:H6	1.78	0.49
6:A:1458:G:H2'	6:A:1459:G:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:D:71:TYR:CG	9:D:199:TYR:HD2	2.30	0.49
39:i:72:LYS:HE2	39:i:101:GLU:OE1	2.12	0.49
43:m:4:ILE:HD11	58:h:2975:G:H4'	1.95	0.49
58:h:2376:G:H2'	58:h:2377:G:H8	1.77	0.49
2:3:9:ARG:O	2:3:12:LYS:HB3	2.13	0.49
5:7:444:PRO:HG3	5:7:476:ARG:H	1.78	0.49
6:A:190:U:H2'	6:A:191:C:C6	2.47	0.49
10:E:176:GLU:CD	10:E:198:ARG:HH22	2.21	0.49
14:I:41:LEU:HD12	14:I:42:VAL:H	1.77	0.49
20:O:82:ILE:HG13	20:O:83:GLU:N	2.27	0.49
27:V:8:GLN:O	27:V:12:SER:HB3	2.12	0.49
39:i:41:GLY:O	39:i:43:ARG:NH1	2.46	0.49
43:m:71:THR:HG21	58:h:2971:G:H5'	1.94	0.49
44:n:41:ARG:HD2	58:h:306:U:H5''	1.95	0.49
56:z:95:ARG:HG3	56:z:101:PHE:CD2	2.48	0.49
58:h:301:U:H5'	58:h:302:U:O5'	2.13	0.49
58:h:1859:A:H2'	58:h:1860:G:O4'	2.13	0.49
58:h:2386:U:OP1	58:h:2393:A:O2'	2.30	0.49
58:h:3071:A:N7	58:h:3089:A:O2'	2.39	0.49
5:7:455:LYS:HZ3	17:L:34:CYS:C	2.21	0.49
6:A:863:G:P	17:L:9:ARG:HH22	2.36	0.49
6:A:1414:C:H2'	6:A:1415:G:O4'	2.12	0.49
9:D:165:TRP:CD1	9:D:165:TRP:H	2.29	0.49
42:l:128:GLN:NE2	58:h:2528:G:O5'	2.37	0.49
43:m:3:ARG:HA	43:m:6:LYS:NZ	2.28	0.49
51:u:77:HIS:CE1	58:h:1674:G:C5	3.01	0.49
58:h:543:U:H3'	58:h:544:U:C5'	2.42	0.49
58:h:639:C:O2'	58:h:640:G:H8	1.95	0.49
5:7:214:ASP:N	5:7:214:ASP:OD1	2.46	0.48
5:7:234:ASP:HB3	5:7:237:LEU:HD12	1.95	0.48
6:A:109:G:H2'	6:A:110:U:C6	2.48	0.48
13:H:98:LEU:HD11	13:H:132:TRP:CD1	2.48	0.48
28:W:117:ASP:H	28:W:149:GLU:HG2	1.78	0.48
28:W:190:LEU:O	50:t:55:ASN:ND2	2.46	0.48
48:r:76:TYR:HB2	53:w:72:THR:CG2	2.43	0.48
58:h:673:C:H2'	58:h:674:U:C6	2.48	0.48
58:h:1194:C:H2'	58:h:1195:A:C8	2.48	0.48
58:h:1707:G:H2'	58:h:1708:A:H8	1.78	0.48
5:7:637:LYS:HD3	5:7:638:ILE:H	1.79	0.48
6:A:194:A:N6	22:Q:20:ARG:HH12	2.11	0.48
6:A:254:G:H2'	6:A:255:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:1066:U:H3	6:A:1079:G:H22	1.61	0.48
9:D:189:PRO:O	9:D:190:LEU:HG	2.13	0.48
12:G:54:THR:OG1	12:G:56:THR:OG1	2.22	0.48
21:P:93:LEU:H	21:P:93:LEU:HD12	1.77	0.48
44:n:9:VAL:HG21	44:n:12:LEU:HD12	1.94	0.48
58:h:728:G:H2'	58:h:729:C:C6	2.49	0.48
58:h:1146:A:H2'	58:h:1147:A:C8	2.48	0.48
58:h:2351:A:H2'	58:h:2352:C:H6	1.77	0.48
58:h:2378:U:H3'	58:h:2379:G:H8	1.78	0.48
3:4:7:G:H2'	3:4:8:A:H8	1.78	0.48
5:7:483:THR:HG21	5:7:517:ARG:HD3	1.96	0.48
6:A:449:C:H2'	6:A:450:G:O4'	2.12	0.48
6:A:819:U:H3	6:A:829:G:H1	1.61	0.48
6:A:904:G:H2'	6:A:905:A:H8	1.77	0.48
6:A:1149:C:O2'	6:A:1150:A:OP2	2.24	0.48
14:I:50:LEU:HB3	14:I:87:LEU:HD11	1.94	0.48
17:L:50:ARG:HG3	17:L:90:LEU:HD21	1.95	0.48
21:P:96:LYS:HD3	21:P:97:GLU:N	2.28	0.48
42:l:82:ALA:C	42:l:85:LYS:H	2.21	0.48
58:h:1005:A:H2'	58:h:1006:G:O4'	2.12	0.48
6:A:437:U:H2'	6:A:438:U:O4'	2.13	0.48
6:A:1132:U:O2'	6:A:1133:G:H5''	2.14	0.48
10:E:191:PRO:HD2	10:E:194:MET:CE	2.43	0.48
40:j:42:THR:OG1	40:j:89:GLU:OE2	2.17	0.48
49:s:105:ARG:HH11	58:h:720:C:N4	2.10	0.48
53:w:48:ARG:NH2	58:h:2909:G:OP1	2.40	0.48
58:h:290:C:H2'	58:h:301:U:C5	2.47	0.48
58:h:1157:G:H1	58:h:1234:U:H3	1.62	0.48
58:h:1542:A:H2'	58:h:1543:A:H8	1.77	0.48
58:h:1656:A:H2'	58:h:1657:G:C8	2.49	0.48
58:h:1963:G:H2'	58:h:1964:U:H6	1.78	0.48
6:A:84:U:H3'	6:A:85:C:H6	1.78	0.48
6:A:397:A:N7	6:A:527:A:O2'	2.43	0.48
6:A:948:G:O2'	14:I:149:LYS:O	2.32	0.48
16:K:44:THR:HA	16:K:50:VAL:HA	1.95	0.48
17:L:76:GLU:OE1	17:L:77:HIS:ND1	2.34	0.48
42:l:170:ASP:OD1	42:l:171:ALA:N	2.47	0.48
47:q:113:LYS:HD3	58:h:615:A:H5'	1.94	0.48
53:w:33:GLU:O	53:w:36:LYS:HG2	2.13	0.48
58:h:2761:U:H2'	58:h:2762:C:C6	2.48	0.48
5:7:678:ALA:O	46:p:31:GLY:HA3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:532:U:H2'	6:A:533:G:H8	1.78	0.48
15:J:87:LEU:HD23	15:J:90:ILE:HD12	1.95	0.48
27:V:61:VAL:HG13	27:V:224:GLY:HA3	1.94	0.48
28:W:7:ILE:H	28:W:7:ILE:HD12	1.78	0.48
46:p:81:LEU:HD21	46:p:134:ALA:HB2	1.94	0.48
49:s:94:GLY:H	49:s:97:GLU:CD	2.22	0.48
58:h:701:A:H2'	58:h:702:A:C8	2.49	0.48
58:h:1542:A:H2'	58:h:1543:A:C8	2.49	0.48
58:h:2510:A:H4'	58:h:2511:A:O4'	2.13	0.48
58:h:2569:G:N3	58:h:2605:C:H2'	2.28	0.48
5:7:581:LYS:HD3	5:7:622:GLN:HE21	1.79	0.48
6:A:23:C:H5''	10:E:116:ALA:HB3	1.95	0.48
6:A:1349:C:O2'	15:J:62:ARG:NH1	2.47	0.48
8:C:119:VAL:HG13	8:C:132:ALA:HB1	1.94	0.48
41:k:160:ARG:NH1	58:h:706:G:HO2'	2.11	0.48
47:q:27:ARG:NH2	58:h:1260:C:O2'	2.46	0.48
55:y:75:ILE:HB	55:y:88:GLN:HB3	1.94	0.48
58:h:138:A:N3	58:h:1523:U:O2'	2.34	0.48
58:h:855:C:H5'	58:h:2001:A:H3'	1.95	0.48
58:h:1550:G:H1	58:h:1620:U:H3	1.61	0.48
5:7:26:VAL:HG22	5:7:114:CYS:HB3	1.95	0.48
6:A:492:U:H2'	6:A:493:A:H8	1.78	0.48
6:A:727:U:H2'	6:A:728:A:O4'	2.14	0.48
6:A:1253:U:H2'	6:A:1254:G:O4'	2.13	0.48
12:G:74:GLU:OE2	12:G:95:ARG:NH1	2.46	0.48
43:m:7:GLN:HB2	43:m:70:ARG:NH1	2.28	0.48
58:h:489:A:H2'	58:h:490:A:C8	2.49	0.48
58:h:1515:C:H2'	58:h:1516:G:C8	2.49	0.48
6:A:485:G:O2'	6:A:486:G:OP1	2.29	0.48
6:A:589:A:C5	6:A:590:A:C8	3.02	0.48
6:A:1411:A:H2'	6:A:1412:C:C6	2.48	0.48
9:D:49:GLN:HB3	9:D:198:LEU:HB2	1.96	0.48
27:V:10:LEU:HD23	27:V:15:HIS:CD2	2.49	0.48
56:z:69:GLU:HB2	56:z:71:LEU:HG	1.94	0.48
58:h:979:G:H2'	58:h:980:C:C6	2.49	0.48
4:5:80:VAL:HG21	4:5:123:ALA:HB2	1.95	0.48
5:7:324:VAL:HG11	5:7:421:ALA:HB1	1.94	0.48
5:7:638:ILE:HD13	5:7:639:ASN:H	1.79	0.48
6:A:312:C:H2'	6:A:313:A:C8	2.49	0.48
6:A:1269:A:H2	6:A:1335:G:H1'	1.79	0.48
58:h:2622:C:H2'	58:h:2623:A:H8	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:1231:A:H2'	6:A:1232:A:C8	2.48	0.47
24:S:38:SER:O	24:S:71:LEU:HD23	2.14	0.47
28:W:175:GLU:OE1	28:W:175:GLU:N	2.47	0.47
43:m:4:ILE:O	43:m:70:ARG:HG2	2.14	0.47
51:u:10:LEU:HD12	51:u:10:LEU:HA	1.74	0.47
52:v:82:VAL:O	52:v:86:GLN:HG3	2.14	0.47
58:h:691:U:H2'	58:h:692:C:C6	2.49	0.47
58:h:996:G:H2'	58:h:997:G:C8	2.45	0.47
58:h:1715:A:H2'	58:h:1716:A:C8	2.49	0.47
58:h:2412:U:H2'	58:h:2413:G:H8	1.78	0.47
5:7:397:LEU:HD22	5:7:402:ARG:HD3	1.94	0.47
5:7:444:PRO:HG2	5:7:476:ARG:HB3	1.95	0.47
6:A:407:A:OP1	9:D:107:ARG:NH1	2.47	0.47
6:A:822:U:H2'	6:A:824:C:H1'	1.96	0.47
14:I:45:THR:OG1	14:I:46:GLY:N	2.43	0.47
18:M:16:GLU:HB3	18:M:41:LYS:HB2	1.96	0.47
27:V:10:LEU:HD23	27:V:15:HIS:HD2	1.78	0.47
50:t:17:GLN:HG3	58:h:1075:U:O4	2.15	0.47
57:1:8:THR:O	57:1:74:VAL:HG12	2.14	0.47
58:h:974:G:O2'	58:h:975:U:P	2.72	0.47
58:h:1146:A:N3	58:h:2710:G:O2'	2.41	0.47
58:h:2289:C:H2'	58:h:2290:C:C6	2.50	0.47
58:h:2368:C:H2'	58:h:2370:A:C6	2.48	0.47
58:h:3007:G:H2'	58:h:3008:C:C6	2.49	0.47
3:4:22:A:O2'	6:A:1177:A:N6	2.47	0.47
6:A:1013:G:H2'	6:A:1014:U:C4'	2.44	0.47
8:C:62:ARG:HH21	8:C:99:GLN:HB3	1.79	0.47
20:O:12:LEU:HG	20:O:31:LEU:HD21	1.96	0.47
45:o:94:LYS:HE2	45:o:121:GLU:HA	1.94	0.47
45:o:115:LEU:HB3	45:o:119:ASP:HB2	1.96	0.47
58:h:273:A:H62	58:h:313:G:H21	1.61	0.47
58:h:1952:C:H2'	58:h:1953:C:C6	2.49	0.47
58:h:3020:U:O2'	58:h:3021:A:O5'	2.28	0.47
58:h:3055:G:H2'	58:h:3100:A:H61	1.79	0.47
6:A:252:U:H2'	6:A:253:U:C6	2.49	0.47
6:A:1514:G:H2'	6:A:1515:A:C8	2.49	0.47
15:J:51:VAL:HG13	19:N:41:ARG:HB2	1.96	0.47
17:L:57:LEU:HD21	17:L:82:VAL:HG21	1.95	0.47
18:M:49:THR:HB	18:M:52:GLN:HG3	1.97	0.47
45:o:105:ILE:HB	45:o:117:VAL:HG13	1.96	0.47
46:p:15:ILE:HD11	46:p:22:PRO:HG3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:p:24:PRO:HD2	46:p:25:PRO:HD3	1.95	0.47
51:u:26:THR:HG23	51:u:75:VAL:HG21	1.95	0.47
58:h:999:C:H2'	58:h:1000:C:O4'	2.14	0.47
58:h:1201:G:H2'	58:h:1202:A:H2'	1.96	0.47
58:h:1204:A:H4'	58:h:1205:G:C8	2.49	0.47
58:h:1659:U:H2'	58:h:1660:A:H8	1.79	0.47
58:h:1900:C:H2'	58:h:1901:C:C6	2.49	0.47
58:h:2365:A:H2'	58:h:2366:C:C6	2.49	0.47
58:h:2401:U:H2'	58:h:2402:C:C6	2.49	0.47
6:A:79:C:H2'	6:A:80:C:C6	2.50	0.47
6:A:481:G:H1'	6:A:529:C:H1'	1.97	0.47
9:D:13:ARG:HD2	9:D:31:TYR:O	2.14	0.47
12:G:75:VAL:HG13	12:G:86:GLN:HB3	1.96	0.47
12:G:75:VAL:HG11	12:G:86:GLN:HE21	1.79	0.47
22:Q:73:ARG:HB3	22:Q:95:GLU:HB3	1.96	0.47
25:T:4:ILE:O	25:T:8:ILE:HG13	2.13	0.47
26:U:57:VAL:HG12	26:U:84:VAL:HG13	1.95	0.47
40:j:169:ARG:NH2	58:h:3046:C:H41	2.13	0.47
56:z:72:ASP:OD1	56:z:74:SER:OG	2.30	0.47
58:h:781:C:H2'	58:h:782:U:C6	2.50	0.47
58:h:954:U:H2'	58:h:955:C:C6	2.50	0.47
58:h:1543:A:N1	58:h:1628:A:O2'	2.40	0.47
58:h:1716:A:H2'	58:h:1718:C:C5	2.50	0.47
58:h:2622:C:H2'	58:h:2623:A:C8	2.49	0.47
5:7:189:VAL:HG22	5:7:196:TYR:HB2	1.97	0.47
5:7:232:SER:HA	5:7:262:ARG:HH22	1.80	0.47
6:A:407:A:O4'	9:D:111:GLN:NE2	2.45	0.47
6:A:408:G:H4'	9:D:104:ARG:HH22	1.80	0.47
33:b:16:ARG:NH1	58:h:1379:G:OP1	2.43	0.47
42:l:18:GLU:N	42:l:18:GLU:OE1	2.48	0.47
45:o:50:THR:O	45:o:79:ILE:N	2.41	0.47
58:h:1195:A:N6	58:h:1206:A:O2'	2.41	0.47
58:h:1614:G:H2'	58:h:1615:G:C8	2.50	0.47
58:h:2058:U:C2	58:h:2059:G:C8	3.02	0.47
58:h:2815:C:H2'	58:h:2816:G:C8	2.49	0.47
2:3:22:PRO:HB3	58:h:1102:G:H2'	1.97	0.47
5:7:668:GLY:HA2	5:7:687:ILE:HG12	1.97	0.47
6:A:426:U:OP1	9:D:31:TYR:OH	2.26	0.47
6:A:465:G:O2'	6:A:466:U:H6	1.98	0.47
6:A:532:U:C2	6:A:533:G:C8	3.03	0.47
6:A:903:U:O2	10:E:49:VAL:HG22	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:994:C:H2'	6:A:995:A:H8	1.79	0.47
6:A:1098:U:H2'	6:A:1099:C:C6	2.49	0.47
6:A:1370:G:H2'	6:A:1371:C:C6	2.50	0.47
6:A:1384:G:H2'	6:A:1385:C:O4'	2.14	0.47
6:A:1442:G:H5''	25:T:26:SER:OG	2.14	0.47
13:H:25:VAL:O	13:H:61:VAL:HA	2.13	0.47
13:H:101:LEU:HD23	13:H:101:LEU:HA	1.76	0.47
17:L:59:SER:HB2	17:L:61:VAL:HG22	1.97	0.47
19:N:3:LYS:O	19:N:7:VAL:HG23	2.15	0.47
40:j:50:VAL:HG12	40:j:84:LEU:HB3	1.97	0.47
40:j:160:VAL:O	40:j:160:VAL:HG12	2.13	0.47
41:k:82:PRO:HB3	41:k:90:VAL:HG23	1.97	0.47
42:l:149:ASP:OD1	42:l:150:VAL:N	2.47	0.47
44:n:124:ILE:HG22	44:n:125:LYS:H	1.80	0.47
46:p:15:ILE:HG23	46:p:44:TYR:OH	2.13	0.47
58:h:1650:G:H2'	58:h:1651:C:C6	2.50	0.47
58:h:1717:U:H5''	58:h:1718:C:H5	1.79	0.47
58:h:2879:G:O2'	58:h:2888:G:O6	2.32	0.47
5:7:260:VAL:HG12	5:7:291:PRO:HD3	1.97	0.47
6:A:332:G:H2'	6:A:333:C:H6	1.80	0.47
6:A:362:G:H5''	17:L:58:THR:HG21	1.97	0.47
6:A:716:U:H2'	6:A:717:C:H6	1.80	0.47
6:A:786:C:H2'	6:A:787:A:H8	1.79	0.47
15:J:50:CYS:SG	15:J:62:ARG:HD3	2.54	0.47
32:a:8:GLN:HE21	32:a:31:ILE:HA	1.80	0.47
39:i:13:ARG:HD2	58:h:843:G:H4'	1.96	0.47
40:j:6:ILE:HD11	40:j:31:ALA:HB1	1.97	0.47
42:l:44:ASN:OD1	42:l:160:ASP:HB2	2.15	0.47
44:n:104:ILE:HD12	44:n:104:ILE:H	1.79	0.47
58:h:1544:U:H2'	58:h:1545:C:C6	2.50	0.47
58:h:1944:C:H2'	58:h:1945:U:H6	1.79	0.47
58:h:2467:U:H2'	58:h:2468:U:C6	2.50	0.47
58:h:3115:A:H2'	58:h:3116:C:H6	1.80	0.47
5:7:666:ARG:NH2	5:7:698:ASP:OD2	2.48	0.47
6:A:458:A:H4'	6:A:459:G:O4'	2.15	0.47
6:A:980:G:H1	6:A:1023:U:H3	1.62	0.47
6:A:1500:G:N2	6:A:1503:A:OP2	2.46	0.47
17:L:42:PRO:HB3	17:L:89:ASP:HB3	1.97	0.47
58:h:2326:A:N6	58:h:2410:A:C6	2.83	0.47
5:7:302:PHE:CE2	5:7:437:ARG:HG2	2.50	0.47
5:7:337:SER:HB2	5:7:418:LEU:HD12	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:243:A:N1	6:A:281:G:O2'	2.41	0.47
6:A:403:C:OP1	9:D:129:SER:HB3	2.15	0.47
6:A:452:A:N6	21:P:94:LYS:H	2.13	0.47
6:A:505:C:H5''	17:L:88:LYS:HE3	1.97	0.47
6:A:994:C:H2'	6:A:995:A:C8	2.50	0.47
23:R:37:LEU:O	23:R:40:THR:OG1	2.32	0.47
32:a:8:GLN:NE2	32:a:30:LYS:O	2.48	0.47
42:l:139:LEU:HD12	42:l:139:LEU:HA	1.67	0.47
48:r:8:LEU:HD22	48:r:84:ALA:HB2	1.97	0.47
58:h:137:G:H2'	58:h:138:A:C8	2.50	0.47
58:h:1537:U:H2'	58:h:1538:G:C8	2.49	0.47
58:h:2873:U:H2'	58:h:2874:C:H6	1.80	0.47
3:4:8:A:H2'	3:4:9:G:H8	1.81	0.46
5:7:41:GLU:HG3	5:7:61:THR:HG22	1.97	0.46
5:7:461:LEU:HD11	5:7:503:LEU:HD21	1.96	0.46
6:A:29:C:H5'	6:A:504:G:HO2'	1.80	0.46
6:A:413:G:H2'	6:A:428:G:H21	1.80	0.46
6:A:1337:A:H2'	6:A:1338:G:C8	2.50	0.46
9:D:80:LYS:HD3	9:D:83:ASP:OD2	2.15	0.46
9:D:133:SER:N	9:D:136:ASP:OD2	2.46	0.46
24:S:42:PRO:O	24:S:45:ILE:HD12	2.15	0.46
34:c:44:ASN:OD1	34:c:45:CYS:N	2.47	0.46
39:i:76:ASN:HB2	39:i:98:LEU:HD22	1.97	0.46
42:l:79:LYS:HG2	42:l:80:SER:H	1.80	0.46
6:A:84:U:H3'	6:A:85:C:C6	2.51	0.46
6:A:493:A:H2'	6:A:494:C:C6	2.50	0.46
6:A:1488:G:OP1	6:A:1491:A:H4'	2.15	0.46
8:C:72:PRO:HD3	8:C:104:GLU:HG2	1.96	0.46
43:m:88:MET:HB2	43:m:132:PHE:CE1	2.50	0.46
48:r:47:ILE:HG22	48:r:50:GLY:H	1.81	0.46
58:h:2:A:H2'	58:h:3:A:C8	2.51	0.46
58:h:672:C:H2'	58:h:673:C:H6	1.80	0.46
58:h:965:U:H2'	58:h:966:U:H6	1.80	0.46
58:h:1553:C:H5''	58:h:1554:U:C5	2.48	0.46
6:A:582:U:H2'	6:A:583:C:C6	2.50	0.46
12:G:58:PRO:HA	12:G:61:THR:HG22	1.97	0.46
12:G:69:VAL:HG11	12:G:134:SER:HB2	1.98	0.46
22:Q:72:ASP:O	22:Q:74:VAL:HG23	2.15	0.46
42:l:110:LEU:HD12	42:l:114:ALA:HB3	1.98	0.46
58:h:443:C:H2'	58:h:444:U:O4'	2.15	0.46
58:h:1436:C:O2'	58:h:1437:A:OP1	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:h:2738:U:H2'	58:h:2739:C:C6	2.51	0.46
6:A:437:U:OP1	9:D:147:THR:OG1	2.34	0.46
6:A:1050:U:H2'	6:A:1051:C:C6	2.50	0.46
44:n:88:THR:HG22	44:n:90:LYS:HG3	1.96	0.46
55:y:72:LYS:HD2	55:y:91:ARG:HG3	1.98	0.46
58:h:222:A:O2'	58:h:508:G:N3	2.47	0.46
58:h:586:U:H2'	58:h:587:G:O4'	2.15	0.46
58:h:844:G:O2'	58:h:878:G:H4'	2.15	0.46
58:h:974:G:O2'	58:h:975:U:O5'	2.31	0.46
1:2:21:A:N6	1:2:46:G:O2'	2.48	0.46
1:2:50:U:H2'	1:2:51:U:H6	1.80	0.46
5:7:176:TYR:CE2	5:7:281:GLU:HB2	2.51	0.46
5:7:521:ARG:HD2	5:7:716:TYR:CE2	2.50	0.46
6:A:13:G:H5'	10:E:133:GLY:HA3	1.97	0.46
6:A:263:A:H2'	6:A:264:U:C6	2.51	0.46
6:A:390:U:H2'	6:A:391:G:H8	1.80	0.46
9:D:139:ASP:OD1	9:D:140:VAL:N	2.45	0.46
17:L:5:GLN:HB2	22:Q:51:LYS:HZ2	1.79	0.46
21:P:21:ILE:HD11	21:P:33:ALA:HB1	1.98	0.46
31:Z:56:ARG:O	31:Z:60:VAL:HG12	2.15	0.46
32:a:29:LYS:NZ	58:h:1048:A:OP1	2.42	0.46
38:g:14:VAL:HG22	38:g:33:ILE:HB	1.98	0.46
38:g:28:LYS:NZ	42:l:147:GLU:HA	2.30	0.46
44:n:80:LEU:N	44:n:147:ASN:O	2.43	0.46
58:h:489:A:H2'	58:h:490:A:H8	1.80	0.46
58:h:2443:U:H2'	58:h:2444:C:C6	2.50	0.46
1:2:34:C:H5'	6:A:948:G:N2	2.31	0.46
5:7:49:VAL:HG23	5:7:83:LEU:HD13	1.97	0.46
5:7:520:LEU:HD21	5:7:640:LEU:HB3	1.97	0.46
5:7:663:LEU:O	5:7:667:ARG:N	2.48	0.46
6:A:272:C:H2'	6:A:273:A:H8	1.81	0.46
6:A:592:U:C2	6:A:593:C:C5	3.03	0.46
6:A:1117:U:H1'	6:A:1118:A:H5''	1.97	0.46
6:A:1183:U:O2'	19:N:27:CYS:SG	2.64	0.46
6:A:1259:G:H8	8:C:26:LYS:NZ	2.14	0.46
9:D:91:SER:HB3	9:D:131:ARG:HG3	1.95	0.46
30:Y:4:VAL:HA	30:Y:10:LYS:O	2.14	0.46
57:1:1:MET:HE2	57:1:68:VAL:HG21	1.98	0.46
58:h:385:G:H2'	58:h:386:C:C6	2.51	0.46
58:h:911:U:H2'	58:h:912:C:C6	2.50	0.46
58:h:1500:A:O2'	58:h:1511:U:O2	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:7:106:ARG:HB3	5:7:439:TRP:CD1	2.51	0.46
13:H:38:GLU:HG3	13:H:49:TYR:OH	2.16	0.46
24:S:43:ASP:N	24:S:43:ASP:OD1	2.49	0.46
30:Y:31:PRO:HB2	30:Y:33:ILE:HG13	1.97	0.46
35:d:6:ARG:O	35:d:9:GLN:NE2	2.47	0.46
45:o:58:LYS:HG2	45:o:70:ASP:OD1	2.15	0.46
47:q:125:TYR:HH	47:q:132:HIS:HE2	1.59	0.46
52:v:37:ARG:NH1	52:v:103:ASP:OD2	2.47	0.46
58:h:740:A:O2'	58:h:741:G:OP2	2.30	0.46
58:h:818:U:H2'	58:h:819:G:O4'	2.15	0.46
58:h:2323:G:H2'	58:h:2324:A:H8	1.81	0.46
3:4:5:A:H2'	3:4:6:G:H8	1.81	0.46
5:7:458:GLU:HG2	17:L:77:HIS:NE2	2.31	0.46
5:7:686:GLU:CD	5:7:715:ARG:HH12	2.24	0.46
6:A:1021:U:H2'	6:A:1022:G:O4'	2.15	0.46
10:E:135:ALA:HB1	10:E:162:VAL:HG23	1.98	0.46
11:F:47:ARG:HH12	11:F:56:ALA:HB1	1.81	0.46
15:J:101:GLN:OE1	15:J:101:GLN:N	2.49	0.46
34:c:9:PRO:HD2	34:c:27:LYS:O	2.16	0.46
38:g:26:SER:OG	38:g:27:THR:N	2.48	0.46
44:n:109:GLY:N	44:n:110:PRO:HD2	2.30	0.46
49:s:6:LEU:HD23	49:s:6:LEU:HA	1.78	0.46
49:s:22:VAL:HG23	49:s:29:LYS:HD2	1.98	0.46
53:w:102:LEU:C	53:w:103:ARG:HD3	2.41	0.46
54:x:28:ARG:HE	58:h:619:C:H2'	1.80	0.46
58:h:302:U:H4'	58:h:303:G:OP1	2.15	0.46
58:h:429:A:H2'	58:h:430:A:C8	2.51	0.46
58:h:997:G:N2	58:h:1011:A:N1	2.64	0.46
58:h:1223:U:C2	58:h:1224:G:C8	3.04	0.46
5:7:176:TYR:CD1	5:7:190:GLY:HA2	2.50	0.46
6:A:452:A:O2'	6:A:453:G:OP1	2.33	0.46
6:A:1370:G:H2'	6:A:1371:C:H6	1.81	0.46
8:C:38:ILE:O	8:C:42:LEU:HG	2.15	0.46
8:C:109:GLU:HB2	8:C:143:GLN:OE1	2.16	0.46
10:E:63:ILE:HD12	10:E:63:ILE:N	2.30	0.46
18:M:95:GLY:O	18:M:96:LEU:HD23	2.16	0.46
38:g:38:CYS:H	38:g:41:CYS:HB2	1.81	0.46
46:p:73:LYS:NZ	58:h:1177:G:OP1	2.44	0.46
51:u:7:GLY:O	51:u:9:ARG:NH1	2.49	0.46
58:h:334:G:N2	58:h:347:U:O2	2.39	0.46
58:h:947:U:H2'	58:h:948:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:h:1003:A:OP1	58:h:1003:A:H2'	2.15	0.46
58:h:2304:C:H2'	58:h:2305:A:C8	2.48	0.46
58:h:2350:G:O2'	58:h:2351:A:OP1	2.28	0.46
1:2:50:U:H2'	1:2:51:U:C6	2.51	0.46
6:A:392:C:H2'	6:A:393:A:H8	1.81	0.46
9:D:182:GLU:O	9:D:186:ILE:HD12	2.15	0.46
24:S:3:ARG:HH21	24:S:7:LYS:HD3	1.82	0.46
40:j:65:PRO:O	40:j:69:GLN:HG3	2.16	0.46
41:k:45:LYS:HD2	58:h:709:U:O4	2.15	0.46
42:l:15:TYR:OH	42:l:36:PRO:O	2.33	0.46
45:o:4:ALA:O	45:o:8:THR:HG23	2.16	0.46
58:h:321:G:H2'	58:h:322:A:H8	1.82	0.46
58:h:1145:A:H61	58:h:1245:U:H5	1.64	0.46
58:h:1529:U:H3'	58:h:1530:G:C8	2.50	0.46
58:h:1963:G:H2'	58:h:1964:U:C6	2.50	0.46
58:h:2323:G:H1	58:h:2412:U:H3	1.64	0.46
5:7:303:THR:HG23	5:7:309:ARG:HB2	1.98	0.45
5:7:698:ASP:O	5:7:702:MET:HG3	2.15	0.45
6:A:1050:U:H2'	6:A:1051:C:H6	1.80	0.45
9:D:186:ILE:HD12	9:D:186:ILE:H	1.81	0.45
14:I:41:LEU:HD11	14:I:81:PHE:HD2	1.80	0.45
16:K:63:GLY:O	16:K:66:LYS:HG2	2.16	0.45
25:T:46:LYS:HE2	25:T:46:LYS:HB2	1.64	0.45
27:V:30:PHE:O	27:V:42:ASP:HB2	2.16	0.45
5:7:106:ARG:HB3	5:7:439:TRP:HD1	1.81	0.45
5:7:521:ARG:HD2	5:7:716:TYR:HE2	1.82	0.45
6:A:255:G:H2'	6:A:256:U:C6	2.52	0.45
6:A:323:U:H2'	6:A:324:G:O4'	2.15	0.45
6:A:1125:G:N2	6:A:1127:A:H62	2.15	0.45
6:A:1156:G:H2'	6:A:1157:A:H8	1.80	0.45
6:A:1393:G:H2'	6:A:1394:U:H6	1.81	0.45
7:B:113:G:H2'	7:B:114:A:H8	1.79	0.45
9:D:186:ILE:HG22	9:D:188:VAL:HG13	1.98	0.45
16:K:128:ASN:HD22	16:K:128:ASN:HA	1.64	0.45
18:M:51:ASP:O	18:M:54:THR:OG1	2.25	0.45
39:i:26:ARG:HD3	39:i:83:GLU:OE1	2.16	0.45
45:o:27:GLU:HB3	45:o:104:VAL:H	1.81	0.45
46:p:29:ALA:HA	46:p:32:GLN:NE2	2.32	0.45
58:h:2365:A:N1	58:h:2373:G:N1	2.64	0.45
58:h:2376:G:H2'	58:h:2377:G:C8	2.51	0.45
58:h:2552:A:H2'	58:h:2553:G:H8	1.77	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:h:2922:U:H2'	58:h:2923:C:H6	1.81	0.45
6:A:504:G:H2'	6:A:505:C:C5	2.52	0.45
6:A:708:A:H2'	6:A:709:A:H8	1.79	0.45
12:G:113:GLU:HG2	12:G:113:GLU:O	2.17	0.45
21:P:100:PRO:HB2	21:P:105:LEU:HD11	1.98	0.45
40:j:6:ILE:HD12	40:j:31:ALA:HB1	1.98	0.45
41:k:101:ARG:O	58:h:774:G:H4'	2.16	0.45
42:l:129:PHE:CE1	42:l:135:TYR:HB2	2.51	0.45
51:u:42:ARG:NH2	58:h:3038:C:OP1	2.48	0.45
58:h:256:A:H2'	58:h:257:A:C8	2.51	0.45
58:h:829:U:O2'	58:h:831:A:N7	2.44	0.45
58:h:980:C:O2'	58:h:981:U:O5'	2.31	0.45
58:h:1326:G:H1'	58:h:1352:A:N6	2.31	0.45
58:h:2553:G:H2'	58:h:2554:U:C6	2.51	0.45
58:h:2873:U:H2'	58:h:2874:C:C6	2.51	0.45
1:2:51:U:H3	1:2:63:G:H1	1.63	0.45
5:7:217:ILE:O	5:7:221:ARG:HG3	2.16	0.45
6:A:668:G:H5'	16:K:58:HIS:HA	1.97	0.45
6:A:1100:U:H2'	6:A:1101:C:C6	2.51	0.45
6:A:1206:U:O2	6:A:1206:U:H2'	2.15	0.45
6:A:1338:G:H2'	6:A:1339:A:H8	1.78	0.45
39:i:186:ASP:OD1	39:i:187:VAL:N	2.50	0.45
40:j:153:GLY:O	58:h:2276:G:H4'	2.17	0.45
42:l:9:PRO:HG3	42:l:101:ASP:HB2	1.98	0.45
57:1:5:LYS:HG3	57:1:24:LEU:O	2.16	0.45
58:h:860:G:O2'	58:h:863:G:O2'	2.20	0.45
58:h:1679:A:H4'	58:h:1679:A:OP1	2.17	0.45
58:h:2378:U:H2'	58:h:2379:G:O4'	2.16	0.45
58:h:2781:G:H2'	58:h:2782:C:C6	2.52	0.45
1:2:63:G:H2'	1:2:64:A:C8	2.51	0.45
6:A:209:A:N3	6:A:222:U:O2'	2.41	0.45
6:A:472:C:H2'	6:A:473:A:H8	1.79	0.45
18:M:72:ARG:NH2	42:l:120:ASP:OD2	2.50	0.45
22:Q:60:LYS:HZ1	22:Q:85:THR:HG21	1.81	0.45
38:g:5:ILE:HG13	42:l:71:LYS:HD3	1.98	0.45
41:k:129:GLU:OE2	41:k:132:GLU:HA	2.17	0.45
49:s:79:ASN:HA	49:s:113:LEU:O	2.16	0.45
58:h:929:C:H2'	58:h:930:C:H6	1.81	0.45
58:h:1472:C:H2'	58:h:1473:G:O4'	2.16	0.45
58:h:2070:A:H2'	58:h:2071:A:C8	2.52	0.45
6:A:1271:A:H2'	6:A:1272:G:H5'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:D:72:GLU:OE1	9:D:72:GLU:HA	2.16	0.45
10:E:90:GLU:OE1	10:E:93:ARG:NH1	2.50	0.45
12:G:38:LEU:O	12:G:42:ILE:HG13	2.17	0.45
16:K:89:LYS:HE2	16:K:89:LYS:HB2	1.81	0.45
40:j:160:VAL:HG21	58:h:2842:G:H21	1.81	0.45
41:k:117:ASP:OD1	41:k:117:ASP:C	2.59	0.45
44:n:101:VAL:HG23	44:n:112:LEU:HB2	1.97	0.45
51:u:65:GLU:HA	51:u:68:LYS:HD2	1.98	0.45
52:v:38:LEU:HD23	52:v:102:PHE:HD1	1.81	0.45
53:w:1:MET:HB3	58:h:3096:U:O2'	2.17	0.45
54:x:91:ASP:OD1	54:x:94:ASN:ND2	2.50	0.45
58:h:639:C:O2'	58:h:640:G:O5'	2.34	0.45
58:h:898:A:N3	58:h:899:G:H5''	2.31	0.45
58:h:1640:A:H2'	58:h:1642:G:N7	2.32	0.45
58:h:1714:A:H2'	58:h:1715:A:C8	2.51	0.45
5:7:225:ILE:HG12	5:7:252:LEU:HD22	1.98	0.45
5:7:225:ILE:HG23	5:7:229:ILE:HD12	1.99	0.45
5:7:475:LEU:HD11	5:7:488:LEU:HD22	1.98	0.45
6:A:252:U:H2'	6:A:253:U:H6	1.82	0.45
6:A:1011:U:O2'	6:A:1012:U:O5'	2.28	0.45
6:A:1125:G:H2'	6:A:1126:G:H5''	1.99	0.45
13:H:10:PHE:HD2	13:H:33:LYS:HD3	1.81	0.45
14:I:134:LYS:HG3	14:I:140:LYS:HA	1.99	0.45
25:T:51:LEU:HD22	25:T:83:LEU:HD23	1.97	0.45
27:V:53:ALA:O	27:V:57:VAL:HG12	2.17	0.45
31:Z:24:GLU:O	31:Z:28:GLU:HG2	2.16	0.45
57:1:96:ARG:C	57:1:97:ILE:HD13	2.42	0.45
58:h:206:A:H2'	58:h:207:C:O4'	2.17	0.45
58:h:1732:U:H2'	58:h:1733:C:C6	2.51	0.45
5:7:220:LEU:HD23	5:7:220:LEU:HA	1.84	0.45
6:A:255:G:H2'	6:A:256:U:H6	1.81	0.45
6:A:592:U:H2'	6:A:593:C:C6	2.51	0.45
6:A:1001:G:H2'	6:A:1002:U:C6	2.52	0.45
6:A:1320:G:H2'	6:A:1321:A:C8	2.52	0.45
6:A:1393:G:H2'	6:A:1394:U:C6	2.52	0.45
35:d:18:VAL:O	35:d:23:LEU:HD22	2.17	0.45
42:l:159:MET:HE3	42:l:159:MET:HB2	1.68	0.45
48:r:92:ASP:N	48:r:92:ASP:OD1	2.47	0.45
58:h:256:A:H2'	58:h:257:A:H8	1.81	0.45
58:h:1043:G:H2'	58:h:1044:U:H6	1.82	0.45
58:h:1165:G:C4	58:h:1228:A:N6	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:h:1250:U:H3'	58:h:1251:A:H5''	1.99	0.45
58:h:1546:A:N1	58:h:1625:G:C6	2.85	0.45
58:h:2113:A:H2'	58:h:2114:A:C8	2.50	0.45
5:7:197:TYR:HD1	5:7:206:ALA:HA	1.81	0.45
6:A:79:C:H2'	6:A:80:C:H6	1.82	0.45
6:A:246:A:C2	6:A:282:A:C5	3.05	0.45
6:A:323:U:H4'	25:T:17:ARG:HB3	1.98	0.45
6:A:728:A:H8	6:A:728:A:OP2	2.00	0.45
6:A:819:U:H3	6:A:829:G:N2	2.14	0.45
6:A:969:G:H2'	6:A:970:G:C8	2.51	0.45
14:I:72:LEU:HA	14:I:75:VAL:HG12	1.99	0.45
20:O:7:GLN:OE1	20:O:7:GLN:N	2.34	0.45
28:W:86:HIS:CE1	28:W:88:ILE:HB	2.52	0.45
33:b:38:LYS:HB2	56:z:41:ASP:OD2	2.17	0.45
40:j:85:ARG:NH2	58:h:2862:G:OP1	2.28	0.45
45:o:36:LEU:O	45:o:40:ARG:HD3	2.16	0.45
52:v:83:ARG:NH1	52:v:87:LEU:HD13	2.32	0.45
57:1:10:LEU:HD23	57:1:80:PRO:HG3	1.99	0.45
58:h:316:U:O2'	58:h:317:G:OP1	2.28	0.45
58:h:997:G:C6	58:h:998:G:C6	3.05	0.45
58:h:1639:G:H5'	58:h:1640:A:OP1	2.17	0.45
58:h:2623:A:H2'	58:h:2624:C:C6	2.51	0.45
5:7:145:VAL:N	5:7:267:PRO:O	2.45	0.45
6:A:1076:C:H2'	6:A:1077:C:H6	1.80	0.45
11:F:27:LEU:HD11	11:F:63:ILE:HG21	1.99	0.45
18:M:52:GLN:HA	18:M:55:VAL:HG22	1.98	0.45
21:P:5:ILE:O	21:P:67:THR:HG23	2.17	0.45
22:Q:79:THR:HG23	22:Q:80:ARG:O	2.17	0.45
29:X:32:LYS:HB3	58:h:759:G:C6	2.51	0.45
32:a:8:GLN:HB2	32:a:28:LEU:HD22	1.99	0.45
36:e:59:ASN:O	36:e:63:ASN:ND2	2.50	0.45
40:j:63:ILE:HG23	40:j:65:PRO:HD2	1.99	0.45
52:v:125:LEU:HD23	52:v:125:LEU:HA	1.76	0.45
58:h:131:A:H2'	58:h:132:C:C6	2.52	0.45
58:h:451:U:H2'	58:h:452:G:C8	2.52	0.45
58:h:483:G:H2'	58:h:484:C:C6	2.52	0.45
58:h:2895:A:C6	58:h:2896:C:C4	3.05	0.45
5:7:520:LEU:HD21	5:7:640:LEU:HD22	1.99	0.44
6:A:928:A:O2'	6:A:1315:A:N3	2.46	0.44
6:A:1181:C:H4'	6:A:1182:A:H5'	1.99	0.44
6:A:1329:G:O2'	6:A:1356:G:O6	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:1350:U:H5'	15:J:62:ARG:NH1	2.32	0.44
7:B:81:U:H2'	7:B:82:A:C8	2.52	0.44
8:C:82:GLU:HA	8:C:85:ARG:HG3	1.99	0.44
8:C:122:GLN:HG2	8:C:127:VAL:HG21	1.99	0.44
8:C:128:ALA:HB1	8:C:130:ARG:HH12	1.81	0.44
12:G:155:ARG:HA	12:G:155:ARG:HD3	1.74	0.44
16:K:103:GLU:HB3	16:K:107:ARG:HH22	1.82	0.44
20:O:12:LEU:HD23	20:O:27:ALA:HB1	1.99	0.44
23:R:49:ARG:HG2	23:R:49:ARG:NH1	2.31	0.44
23:R:49:ARG:HG2	23:R:49:ARG:HH11	1.81	0.44
25:T:32:ILE:HD11	25:T:75:LYS:HG2	1.98	0.44
49:s:105:ARG:HH11	58:h:720:C:H42	1.65	0.44
53:w:26:ASN:OD1	53:w:84:ASP:HB2	2.17	0.44
58:h:680:U:H2'	58:h:681:C:H6	1.80	0.44
58:h:2125:A:O2'	58:h:2126:C:OP2	2.27	0.44
58:h:2753:G:H5''	58:h:2754:G:H5''	1.98	0.44
5:7:272:CYS:N	5:7:277:VAL:O	2.50	0.44
5:7:357:HIS:CE1	5:7:424:GLY:HA3	2.52	0.44
5:7:458:GLU:HG3	5:7:458:GLU:O	2.17	0.44
6:A:382:A:H2'	6:A:383:A:C8	2.52	0.44
6:A:1394:U:H2'	6:A:1395:C:C6	2.52	0.44
29:X:75:ARG:NH2	58:h:2557:A:OP1	2.50	0.44
31:Z:38:THR:OG1	31:Z:40:GLN:HG3	2.17	0.44
44:n:33:ARG:HB3	44:n:35:LEU:HD13	1.99	0.44
58:h:502:C:H2'	58:h:503:A:C8	2.52	0.44
58:h:703:C:H2'	58:h:704:C:H6	1.81	0.44
58:h:747:A:H2'	58:h:748:U:O4'	2.16	0.44
58:h:1732:U:H2'	58:h:1733:C:H6	1.82	0.44
58:h:2084:A:H2'	58:h:2085:C:O4'	2.18	0.44
58:h:2211:C:H2'	58:h:2212:A:H8	1.80	0.44
58:h:2871:U:H2'	58:h:2872:G:H8	1.82	0.44
5:7:122:ASN:HD22	5:7:154:ARG:HH21	1.65	0.44
6:A:433:C:C2	6:A:434:C:C5	3.06	0.44
6:A:510:G:H2'	6:A:510:G:N3	2.31	0.44
6:A:996:G:N2	6:A:999:A:OP2	2.43	0.44
6:A:1004:G:H2'	6:A:1005:G:H8	1.83	0.44
12:G:101:LEU:HD23	12:G:101:LEU:HA	1.82	0.44
17:L:83:ARG:N	17:L:96:LYS:O	2.49	0.44
21:P:20:ILE:HG22	21:P:37:ILE:HB	2.00	0.44
42:l:11:LEU:HD23	42:l:11:LEU:HA	1.71	0.44
43:m:89:GLU:OE1	43:m:89:GLU:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:n:124:ILE:CG2	44:n:125:LYS:H	2.29	0.44
46:p:59:GLU:HB3	46:p:71:ALA:HB3	1.99	0.44
58:h:1178:U:C2	58:h:1180:G:H5'	2.53	0.44
58:h:1762:C:H2'	58:h:1763:G:O4'	2.17	0.44
58:h:2381:A:H4'	58:h:2382:G:O5'	2.18	0.44
6:A:492:U:H2'	6:A:493:A:C8	2.53	0.44
6:A:847:A:H2'	6:A:848:C:C6	2.52	0.44
7:B:63:U:H2'	7:B:64:G:H8	1.83	0.44
8:C:81:THR:O	8:C:85:ARG:HG3	2.16	0.44
20:O:56:LEU:HD21	58:h:830:A:C2	2.52	0.44
25:T:28:LEU:HD11	25:T:58:LEU:HA	2.00	0.44
25:T:35:PHE:HA	25:T:50:LEU:HD11	1.98	0.44
46:p:93:GLU:HB3	46:p:96:LYS:HB2	2.00	0.44
50:t:108:TYR:CD1	50:t:109:PRO:HD2	2.53	0.44
52:v:38:LEU:HD23	52:v:102:PHE:CD1	2.52	0.44
58:h:31:U:O2'	58:h:32:G:H5'	2.18	0.44
58:h:287:A:P	58:h:287:A:H8	2.39	0.44
58:h:610:C:O2	58:h:646:U:O2'	2.35	0.44
5:7:444:PRO:CG	5:7:476:ARG:HB3	2.47	0.44
6:A:45:G:H2'	6:A:46:G:H8	1.83	0.44
6:A:48:G:OP2	21:P:13:ILE:HB	2.17	0.44
6:A:343:U:O2'	6:A:346:G:O6	2.30	0.44
6:A:375:U:C2	6:A:376:G:C8	3.06	0.44
10:E:140:LEU:CD1	10:E:148:ILE:HD13	2.48	0.44
40:j:89:GLU:HA	40:j:92:VAL:HB	2.00	0.44
40:j:185:VAL:HG12	40:j:192:LEU:HD23	1.99	0.44
47:q:29:ALA:HB3	47:q:108:MET:HE3	2.00	0.44
48:r:34:GLY:HA3	48:r:69:ARG:HH21	1.81	0.44
58:h:193:G:H2'	58:h:194:A:O4'	2.17	0.44
58:h:782:U:H2'	58:h:783:G:O4'	2.18	0.44
58:h:1485:C:H2'	58:h:1486:G:O4'	2.18	0.44
5:7:185:CYS:HB3	5:7:272:CYS:SG	2.58	0.44
5:7:471:GLU:OE1	5:7:506:ARG:NH1	2.51	0.44
5:7:701:SER:HA	58:h:2884:A:N7	2.32	0.44
6:A:523:U:H2'	6:A:524:C:C6	2.52	0.44
8:C:91:GLU:OE1	8:C:91:GLU:HA	2.17	0.44
8:C:138:GLN:O	8:C:142:ARG:HG3	2.16	0.44
9:D:82:GLY:O	9:D:86:LEU:HG	2.17	0.44
27:V:47:LEU:HD13	27:V:47:LEU:HA	1.79	0.44
27:V:83:GLU:O	27:V:87:VAL:HG23	2.18	0.44
41:k:68:GLN:NE2	41:k:75:ARG:HD2	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:l:101:ASP:OD1	42:l:102:ARG:N	2.51	0.44
58:h:1193:C:H2'	58:h:1194:C:H6	1.82	0.44
58:h:2359:G:H1	58:h:2379:G:H1'	1.83	0.44
6:A:1105:U:C2	6:A:1107:G:C8	3.06	0.44
27:V:133:GLU:O	27:V:137:LEU:HG	2.18	0.44
37:f:31:ARG:NH1	58:h:2702:A:OP1	2.51	0.44
58:h:1198:C:H2'	58:h:1199:U:C6	2.53	0.44
58:h:1656:A:H2'	58:h:1657:G:H8	1.82	0.44
6:A:264:U:H2'	6:A:265:G:O4'	2.17	0.44
6:A:491:C:C2	6:A:492:U:C5	3.06	0.44
10:E:157:ASN:O	10:E:161:VAL:HG23	2.18	0.44
15:J:23:ARG:O	15:J:27:GLU:HG2	2.17	0.44
20:O:78:TYR:OH	20:O:89:ARG:O	2.20	0.44
26:U:9:ASP:OD1	26:U:9:ASP:C	2.61	0.44
27:V:52:LYS:HE2	27:V:198:TYR:CE1	2.52	0.44
50:t:68:ILE:HD13	50:t:68:ILE:HA	1.81	0.44
52:v:83:ARG:HD2	52:v:83:ARG:HA	1.76	0.44
58:h:487:U:H2'	58:h:488:G:O4'	2.18	0.44
58:h:965:U:H2'	58:h:966:U:C6	2.51	0.44
58:h:1189:G:N3	58:h:1207:G:O2'	2.40	0.44
58:h:1942:G:H2'	58:h:1943:C:H6	1.82	0.44
5:7:374:ALA:HA	5:7:469:ALA:HB1	2.00	0.44
5:7:643:PRO:HA	5:7:716:TYR:HA	2.00	0.44
6:A:294:C:OP1	6:A:590:A:O2'	2.33	0.44
6:A:631:C:H2'	6:A:632:U:C6	2.53	0.44
6:A:964:U:H4'	6:A:965:A:O4'	2.18	0.44
16:K:93:VAL:HB	16:K:119:ILE:HD12	2.00	0.44
23:R:44:GLU:OE1	23:R:44:GLU:N	2.48	0.44
33:b:35:GLN:N	33:b:35:GLN:OE1	2.51	0.44
40:j:213:LYS:HD3	58:h:2957:A:C4	2.53	0.44
42:l:142:GLN:HB3	42:l:157:ARG:O	2.17	0.44
48:r:71:ARG:HH22	48:r:122:LEU:C	2.25	0.44
52:v:74:ASP:N	52:v:74:ASP:OD1	2.49	0.44
58:h:2359:G:N1	58:h:2379:G:H1'	2.33	0.44
58:h:2895:A:C5	58:h:2896:C:C5	3.05	0.44
5:7:561:GLU:HB3	5:7:603:ARG:HG3	1.99	0.43
5:7:663:LEU:HA	5:7:666:ARG:HB2	2.00	0.43
6:A:321:A:H2'	6:A:322:C:H6	1.83	0.43
6:A:399:G:H2'	6:A:400:C:C6	2.53	0.43
6:A:410:G:H2'	6:A:429:U:C4	2.53	0.43
15:J:77:LEU:HD23	15:J:78:ASP:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:80:ALA:HB2	16:K:109:LEU:HD23	2.00	0.43
34:c:6:ASP:OD1	34:c:7:VAL:N	2.48	0.43
39:i:181:GLU:HB2	39:i:270:ARG:O	2.17	0.43
43:m:95:TYR:HA	43:m:107:ALA:O	2.18	0.43
48:r:110:LYS:HB3	48:r:110:LYS:HE2	1.79	0.43
49:s:95:VAL:O	49:s:99:VAL:HG13	2.17	0.43
52:v:3:HIS:CE1	52:v:5:PRO:HD3	2.53	0.43
53:w:12:LEU:HD23	53:w:12:LEU:HA	1.84	0.43
58:h:113:C:O2'	58:h:123:A:N3	2.47	0.43
58:h:159:A:H2'	58:h:160:A:C8	2.53	0.43
58:h:844:G:H5'	58:h:845:C:H5''	1.98	0.43
58:h:2515:U:H2'	58:h:2516:U:H6	1.82	0.43
6:A:591:C:C2	6:A:592:U:C5	3.07	0.43
6:A:902:U:H2'	6:A:903:U:C6	2.53	0.43
6:A:1110:A:H61	6:A:1125:G:H1'	1.82	0.43
6:A:1296:C:H2'	6:A:1297:U:H6	1.82	0.43
19:N:8:HIS:CD2	19:N:8:HIS:C	2.96	0.43
30:Y:64:ALA:HA	44:n:32:PRO:HB3	2.00	0.43
40:j:155:ALA:H	58:h:2277:G:H5'	1.83	0.43
53:w:71:ARG:HG2	53:w:73:PHE:CZ	2.53	0.43
58:h:113:C:H2'	58:h:114:G:O4'	2.17	0.43
58:h:296:A:N6	58:h:297:G:O6	2.51	0.43
58:h:388:U:H2'	58:h:389:G:O4'	2.18	0.43
58:h:664:A:H5''	58:h:665:G:OP2	2.19	0.43
58:h:1001:C:H1'	58:h:1007:G:N2	2.28	0.43
58:h:1532:G:N2	58:h:1804:G:C4	2.86	0.43
58:h:1541:G:N2	58:h:1631:A:N1	2.66	0.43
58:h:2326:A:H2'	58:h:2327:C:C6	2.53	0.43
58:h:2347:G:O6	58:h:2348:G:N2	2.47	0.43
58:h:2588:C:H2'	58:h:2589:G:O4'	2.19	0.43
58:h:3116:C:H2'	58:h:3117:U:H6	1.83	0.43
5:7:455:LYS:HB3	17:L:33:VAL:HG11	2.00	0.43
6:A:358:U:H2'	6:A:359:G:H8	1.83	0.43
6:A:907:G:C2	6:A:909:G:C8	3.06	0.43
6:A:993:G:H2'	6:A:994:C:C6	2.53	0.43
11:F:26:PHE:CZ	11:F:82:ASN:ND2	2.86	0.43
39:i:60:ARG:HA	58:h:1788:G:H5'	2.00	0.43
41:k:108:ALA:O	41:k:112:ARG:HD3	2.18	0.43
44:n:30:LEU:HB3	44:n:36:ALA:HB3	2.00	0.43
48:r:66:VAL:O	48:r:78:LYS:HG3	2.18	0.43
48:r:105:GLU:HA	48:r:108:GLU:OE1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:y:16:VAL:HB	55:y:99:VAL:HG21	2.01	0.43
56:z:79:ALA:HB2	56:z:115:GLU:HG3	1.99	0.43
58:h:2145:C:H2'	58:h:2146:A:H8	1.83	0.43
58:h:2373:G:H2'	58:h:2374:U:C6	2.54	0.43
58:h:3014:A:N6	58:h:3113:A:OP2	2.51	0.43
6:A:321:A:H2'	6:A:322:C:C6	2.53	0.43
6:A:324:G:N1	6:A:327:A:OP2	2.49	0.43
6:A:590:A:C5	6:A:591:C:C5	3.06	0.43
6:A:654:G:H21	16:K:127:HIS:HB2	1.82	0.43
16:K:102:ARG:HB2	16:K:103:GLU:OE1	2.19	0.43
39:i:21:PHE:HB3	39:i:24:ILE:HG13	2.00	0.43
46:p:115:LYS:HD2	46:p:123:ILE:HG12	1.99	0.43
51:u:94:TYR:O	51:u:116:VAL:HG22	2.18	0.43
56:z:37:GLU:H	56:z:37:GLU:CD	2.26	0.43
58:h:175:G:O2'	58:h:176:G:H5'	2.19	0.43
58:h:340:A:H2'	58:h:341:C:C6	2.54	0.43
58:h:2679:G:H2'	58:h:2680:C:C6	2.54	0.43
5:7:550:GLU:HB3	5:7:605:THR:HB	2.00	0.43
6:A:308:C:C2	6:A:309:G:C8	3.06	0.43
6:A:452:A:H2	21:P:47:SER:HB2	1.84	0.43
6:A:742:A:H2'	6:A:743:G:H8	1.83	0.43
6:A:998:G:H2'	6:A:999:A:C8	2.53	0.43
8:C:164:ARG:NH1	8:C:164:ARG:HB2	2.34	0.43
10:E:175:PRO:HG2	10:E:198:ARG:HH21	1.82	0.43
11:F:11:ASP:N	11:F:84:SER:O	2.52	0.43
11:F:30:ILE:HG22	11:F:36:THR:HG21	1.99	0.43
13:H:105:ILE:HD11	13:H:112:LEU:HD13	2.01	0.43
20:O:85:LEU:HD23	20:O:85:LEU:HA	1.82	0.43
21:P:21:ILE:HA	21:P:21:ILE:HD12	1.75	0.43
25:T:75:LYS:HE2	25:T:75:LYS:HB2	1.85	0.43
49:s:51:GLU:OE1	49:s:56:PRO:HA	2.18	0.43
56:z:65:ALA:HB1	56:z:71:LEU:HD12	2.00	0.43
58:h:131:A:H2'	58:h:132:C:H6	1.84	0.43
58:h:270:U:H1'	58:h:512:G:N2	2.33	0.43
58:h:1400:G:N2	58:h:1443:G:H5''	2.34	0.43
58:h:2096:G:H2'	58:h:2097:G:H8	1.83	0.43
1:2:26:A:N6	1:2:44:G:H1	2.15	0.43
6:A:407:A:H2'	6:A:408:G:C8	2.54	0.43
6:A:490:A:N3	6:A:523:U:H1'	2.34	0.43
6:A:503:A:H61	17:L:89:ASP:HB2	1.84	0.43
6:A:560:C:H2'	6:A:561:G:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:1138:A:N1	6:A:1161:A:N6	2.65	0.43
6:A:1259:G:H8	8:C:26:LYS:HZ3	1.67	0.43
6:A:1382:C:C2	6:A:1486:A:N6	2.87	0.43
8:C:29:LYS:HE3	19:N:38:GLY:HA3	2.00	0.43
10:E:83:ALA:O	10:E:87:LYS:HG2	2.18	0.43
18:M:15:MET:HE2	18:M:15:MET:HB2	1.93	0.43
26:U:4:ILE:O	31:Z:26:LYS:NZ	2.51	0.43
27:V:162:TRP:HE1	27:V:214:THR:HG22	1.84	0.43
29:X:40:GLN:HG3	29:X:42:GLY:O	2.18	0.43
34:c:30:ARG:HG3	34:c:30:ARG:NH1	2.33	0.43
36:e:15:ARG:NH2	36:e:47:ARG:HH21	2.17	0.43
42:l:79:LYS:HG2	42:l:80:SER:N	2.34	0.43
52:v:69:ASP:OD1	52:v:70:VAL:N	2.51	0.43
58:h:1165:G:C2	58:h:1228:A:C5	3.07	0.43
58:h:1529:U:H3'	58:h:1530:G:H8	1.83	0.43
58:h:1626:G:H2'	58:h:1627:U:O4'	2.18	0.43
58:h:1707:G:H2'	58:h:1708:A:C8	2.53	0.43
5:7:176:TYR:CE1	5:7:190:GLY:HA2	2.54	0.43
5:7:587:MET:O	5:7:599:VAL:HG23	2.19	0.43
6:A:120:G:H2'	6:A:121:U:C6	2.54	0.43
6:A:1333:U:H4'	12:G:33:GLU:OE2	2.18	0.43
6:A:1436:G:H3'	6:A:1436:G:OP2	2.17	0.43
8:C:61:ASP:OD1	8:C:61:ASP:N	2.35	0.43
8:C:178:LEU:HA	8:C:178:LEU:HD23	1.83	0.43
17:L:5:GLN:OE1	22:Q:51:LYS:NZ	2.47	0.43
31:Z:18:LEU:HD23	31:Z:18:LEU:HA	1.76	0.43
34:c:35:ARG:HE	34:c:52:LYS:HG2	1.83	0.43
36:e:23:VAL:HG13	36:e:47:ARG:HB3	2.00	0.43
40:j:151:ILE:HD13	40:j:151:ILE:HA	1.84	0.43
42:l:118:ILE:HD13	42:l:144:MET:HG2	1.99	0.43
46:p:131:ALA:HA	46:p:141:VAL:HG11	2.01	0.43
55:y:60:VAL:HG23	55:y:102:ILE:HG13	1.99	0.43
56:z:49:ALA:HB2	58:h:2234:G:H5''	2.00	0.43
58:h:943:U:H2'	58:h:944:A:C8	2.52	0.43
58:h:1944:C:H2'	58:h:1945:U:C6	2.54	0.43
5:7:178:PRO:HD3	5:7:270:PRO:HG3	2.00	0.43
6:A:25:G:H2'	6:A:26:G:C8	2.53	0.43
6:A:1476:A:H5''	17:L:44:LYS:HZ2	1.83	0.43
20:O:55:GLY:O	20:O:59:LEU:HG	2.18	0.43
21:P:5:ILE:HG12	21:P:22:VAL:HG22	2.00	0.43
27:V:57:VAL:O	27:V:61:VAL:HG12	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:111:LEU:HD12	39:i:111:LEU:HA	1.71	0.43
50:t:34:ILE:HD13	50:t:122:ILE:HG13	2.00	0.43
58:h:461:U:H2'	58:h:462:A:H8	1.83	0.43
58:h:981:U:HO2'	58:h:982:A:P	2.35	0.43
58:h:1659:U:H2'	58:h:1660:A:C8	2.54	0.43
58:h:1705:C:H2'	58:h:1706:A:C8	2.48	0.43
58:h:1764:A:H2'	58:h:1765:A:C8	2.54	0.43
58:h:2309:U:H2'	58:h:2310:G:C8	2.53	0.43
5:7:530:GLY:HA3	5:7:632:ALA:HB2	2.00	0.43
6:A:185:G:H1	6:A:203:U:H3	1.65	0.43
6:A:509:G:H5'	6:A:510:G:OP2	2.18	0.43
6:A:1336:C:H2'	6:A:1337:A:H8	1.83	0.43
8:C:27:GLN:OE1	8:C:27:GLN:N	2.51	0.43
12:G:115:THR:HB	12:G:118:GLU:HG3	2.00	0.43
13:H:39:ILE:HD13	13:H:42:ARG:NH2	2.33	0.43
22:Q:27:VAL:HG22	22:Q:38:VAL:HG22	2.01	0.43
22:Q:62:HIS:HB2	22:Q:86:LYS:NZ	2.34	0.43
22:Q:77:MET:HE3	22:Q:91:VAL:HG11	2.01	0.43
27:V:96:TRP:CH2	27:V:101:LEU:HD13	2.53	0.43
46:p:15:ILE:HD13	46:p:26:VAL:HG23	2.00	0.43
58:h:334:G:H2'	58:h:335:G:H8	1.80	0.43
58:h:2096:G:H2'	58:h:2097:G:C8	2.54	0.43
58:h:2366:C:H2'	58:h:2367:G:O4'	2.19	0.43
58:h:2394:A:H5'	58:h:2396:A:N7	2.34	0.43
58:h:2411:U:H2'	58:h:2412:U:O4'	2.19	0.43
6:A:411:A:C6	6:A:429:U:C4	3.07	0.43
6:A:533:G:H2'	6:A:534:U:C6	2.54	0.43
6:A:860:C:H5'	13:H:83:PRO:HG2	2.00	0.43
6:A:1470:G:H2'	6:A:1471:G:O4'	2.19	0.43
12:G:73:LEU:HD12	12:G:73:LEU:HA	1.81	0.43
15:J:15:HIS:O	15:J:18:ILE:HG22	2.19	0.43
17:L:77:HIS:O	17:L:77:HIS:CG	2.71	0.43
39:i:146:GLU:HB2	39:i:189:CYS:HB3	2.00	0.43
46:p:15:ILE:CD1	46:p:25:PRO:HG2	2.49	0.43
46:p:118:LEU:HG	46:p:119:ASN:H	1.83	0.43
48:r:78:LYS:HD3	53:w:70:GLU:OE1	2.19	0.43
58:h:273:A:H62	58:h:313:G:N2	2.17	0.43
58:h:483:G:H2'	58:h:484:C:H6	1.83	0.43
58:h:594:U:H5'	58:h:595:A:H5''	2.01	0.43
58:h:654:U:H6	58:h:654:U:H2'	1.64	0.43
58:h:1334:C:H2'	58:h:1335:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:h:2871:U:H2'	58:h:2872:G:C8	2.54	0.43
58:h:3007:G:H2'	58:h:3008:C:H6	1.84	0.43
5:7:566:VAL:HG22	5:7:608:ASP:C	2.44	0.42
6:A:1132:U:H5''	15:J:44:THR:HG23	2.01	0.42
10:E:105:THR:HG23	10:E:106:ILE:O	2.18	0.42
11:F:89:LYS:HE2	11:F:89:LYS:HB2	1.83	0.42
25:T:20:ARG:NH2	25:T:64:LYS:HB3	2.34	0.42
27:V:52:LYS:HE2	27:V:198:TYR:HE1	1.83	0.42
34:c:6:ASP:OD1	34:c:29:ARG:NH1	2.52	0.42
39:i:272:ARG:O	39:i:273:ARG:NH1	2.52	0.42
42:l:154:ASP:OD1	42:l:155:ARG:N	2.51	0.42
43:m:22:GLN:OE1	43:m:22:GLN:HA	2.19	0.42
43:m:87:LYS:HA	43:m:133:SER:HA	1.99	0.42
46:p:80:LEU:HD23	46:p:80:LEU:HA	1.90	0.42
58:h:445:U:H4'	58:h:446:G:O5'	2.19	0.42
58:h:2007:C:H2'	58:h:2008:A:C8	2.54	0.42
9:D:15:LEU:HD13	9:D:55:LYS:HG2	2.00	0.42
10:E:70:MET:HE3	10:E:70:MET:HB3	1.85	0.42
18:M:65:LYS:HB3	18:M:69:ASP:OD2	2.20	0.42
27:V:111:LEU:HD22	27:V:152:ARG:HA	2.00	0.42
27:V:139:ARG:HD3	27:V:139:ARG:H	1.82	0.42
58:h:1165:G:O2'	58:h:1228:A:N1	2.49	0.42
58:h:2003:A:H1'	58:h:2162:A:N6	2.34	0.42
58:h:2262:C:H2'	58:h:2263:G:O4'	2.19	0.42
6:A:667:A:C2	6:A:684:A:C5	3.07	0.42
6:A:863:G:H2'	6:A:864:C:O4'	2.19	0.42
8:C:23:TYR:HD2	15:J:97:ASP:HB2	1.85	0.42
14:I:80:GLN:HB2	14:I:81:PHE:CE1	2.53	0.42
23:R:34:ASP:HB3	23:R:37:LEU:HB3	2.01	0.42
27:V:47:LEU:HA	27:V:50:ILE:HB	2.02	0.42
28:W:85:VAL:HG13	28:W:91:ASN:O	2.19	0.42
28:W:118:ALA:HB2	28:W:148:VAL:HG22	2.01	0.42
41:k:182:GLN:HE22	58:h:706:G:H1'	1.84	0.42
42:l:177:LEU:HD23	42:l:177:LEU:HA	1.69	0.42
43:m:22:GLN:NE2	43:m:39:GLU:HA	2.35	0.42
43:m:154:ARG:NH1	58:h:2750:G:OP2	2.52	0.42
47:q:55:ILE:HA	47:q:123:LYS:O	2.19	0.42
49:s:31:LYS:HE3	58:h:658:U:C5'	2.45	0.42
58:h:580:G:H2'	58:h:581:G:O4'	2.19	0.42
58:h:1478:C:O2'	58:h:2026:A:N3	2.49	0.42
58:h:1561:C:N3	58:h:1610:C:N4	2.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:h:2777:G:C2	58:h:2807:G:H1'	2.55	0.42
5:7:581:LYS:HD3	5:7:622:GLN:NE2	2.35	0.42
6:A:592:U:H2'	6:A:593:C:H6	1.84	0.42
14:I:118:LEU:HD23	14:I:118:LEU:HA	1.84	0.42
40:j:13:MET:HE3	40:j:13:MET:HB2	1.79	0.42
42:l:76:ARG:HB3	42:l:89:GLY:HA2	2.00	0.42
58:h:2297:U:H2'	58:h:2298:U:H6	1.84	0.42
1:2:4:C:H2'	1:2:5:G:C8	2.54	0.42
5:7:25:ASN:O	5:7:112:ALA:HB1	2.20	0.42
6:A:45:G:H2'	6:A:46:G:C8	2.54	0.42
6:A:105:A:C6	6:A:326:G:C6	3.07	0.42
6:A:1018:C:C2	6:A:1019:U:C5	3.07	0.42
10:E:73:VAL:HG21	10:E:162:VAL:HG11	2.01	0.42
25:T:48:SER:O	25:T:52:HIS:ND1	2.52	0.42
25:T:50:LEU:O	25:T:54:THR:HG23	2.19	0.42
28:W:158:THR:HG22	28:W:161:GLN:OE1	2.20	0.42
53:w:59:THR:OG1	53:w:72:THR:HB	2.19	0.42
58:h:1673:A:C5	58:h:2926:A:C8	3.06	0.42
58:h:1809:U:H2'	58:h:1810:A:C8	2.54	0.42
58:h:2483:G:C8	58:h:2651:C:C4	3.07	0.42
58:h:2581:G:H8	58:h:2581:G:OP2	2.03	0.42
58:h:3045:C:H2'	58:h:3046:C:O4'	2.18	0.42
58:h:3116:C:H2'	58:h:3117:U:C6	2.55	0.42
5:7:701:SER:HB2	58:h:2884:A:N6	2.34	0.42
6:A:360:G:C6	6:A:361:G:C6	3.08	0.42
7:B:115:A:H2'	7:B:116:C:C6	2.54	0.42
11:F:17:ARG:H	11:F:17:ARG:HG2	1.61	0.42
41:k:148:LEU:HD23	41:k:148:LEU:HA	1.81	0.42
42:l:74:VAL:HG11	42:l:91:PRO:HB3	2.02	0.42
42:l:103:MET:O	42:l:107:LEU:HD22	2.19	0.42
51:u:11:GLY:O	51:u:16:HIS:ND1	2.47	0.42
58:h:453:U:H2'	58:h:454:U:C6	2.55	0.42
58:h:565:A:H2'	58:h:566:A:C8	2.55	0.42
58:h:757:G:H4'	58:h:758:A:H5'	2.02	0.42
58:h:2912:A:H5''	58:h:2937:G:O6	2.20	0.42
5:7:532:GLY:HA3	5:7:628:ALA:HB2	2.01	0.42
6:A:264:U:O2'	22:Q:81:PRO:O	2.36	0.42
6:A:545:U:H3'	6:A:546:G:H2'	2.02	0.42
6:A:865:C:O2'	6:A:866:U:H5'	2.19	0.42
6:A:1147:G:H22	6:A:1150:A:H3'	1.84	0.42
6:A:1424:G:H5'	6:A:1425:G:OP1	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:40:A:C2	7:B:45:G:C2	3.08	0.42
10:E:100:PRO:HB3	10:E:174:ARG:HG3	2.00	0.42
10:E:179:ALA:HB1	10:E:184:LEU:O	2.19	0.42
15:J:24:LYS:HZ2	15:J:90:ILE:HG23	1.83	0.42
16:K:110:GLN:OE1	16:K:116:VAL:HG13	2.20	0.42
17:L:30:ARG:O	17:L:81:LEU:HD12	2.20	0.42
18:M:69:ASP:C	18:M:69:ASP:OD1	2.62	0.42
20:O:33:THR:O	20:O:37:GLN:HG3	2.20	0.42
21:P:24:ASP:O	21:P:27:THR:OG1	2.37	0.42
27:V:192:ASP:HB3	27:V:195:VAL:HG22	2.01	0.42
31:Z:18:LEU:HD22	31:Z:57:VAL:HG13	2.01	0.42
36:e:22:ILE:HG21	36:e:58:ILE:HG21	2.02	0.42
47:q:65:SER:OG	58:h:1259:U:OP2	2.37	0.42
51:u:67:MET:HG2	51:u:76:VAL:HG21	2.00	0.42
58:h:502:C:H2'	58:h:503:A:H8	1.83	0.42
58:h:673:C:H2'	58:h:674:U:H6	1.84	0.42
58:h:928:U:H2'	58:h:929:C:H6	1.84	0.42
58:h:977:G:H2'	58:h:978:A:O4'	2.19	0.42
58:h:2814:A:H2'	58:h:2815:C:H6	1.85	0.42
5:7:113:ASP:HB2	5:7:296:HIS:CG	2.55	0.42
6:A:312:C:H2'	6:A:313:A:H8	1.85	0.42
6:A:1007:U:O2'	6:A:1008:C:P	2.78	0.42
6:A:1305:G:H2'	6:A:1306:A:H8	1.84	0.42
7:B:26:A:H2'	7:B:27:A:C8	2.54	0.42
9:D:151:GLN:HA	9:D:154:ARG:HG2	2.00	0.42
14:I:111:GLN:HB3	14:I:113:GLU:OE1	2.20	0.42
22:Q:27:VAL:HG23	22:Q:74:VAL:HG21	2.01	0.42
32:a:21:GLU:OE1	32:a:24:ARG:NH2	2.41	0.42
39:i:222:ARG:NH1	58:h:2044:U:OP2	2.46	0.42
45:o:91:LYS:HB3	45:o:91:LYS:HE3	1.80	0.42
53:w:3:THR:OG1	53:w:4:LEU:N	2.52	0.42
58:h:1172:A:H2'	58:h:1173:G:O4'	2.20	0.42
58:h:1179:U:O2	58:h:1187:A:H5''	2.19	0.42
58:h:1854:U:H2'	58:h:1855:A:C8	2.54	0.42
5:7:43:LEU:HD22	5:7:283:LEU:HG	2.01	0.42
6:A:1230:C:O2'	14:I:95:GLN:NE2	2.32	0.42
6:A:1515:A:H8	6:A:1515:A:O5'	2.03	0.42
9:D:183:ARG:HD2	9:D:183:ARG:HA	1.80	0.42
13:H:14:LEU:HD23	13:H:14:LEU:HA	1.83	0.42
19:N:27:CYS:SG	19:N:29:ARG:HB2	2.60	0.42
20:O:9:LYS:HG3	20:O:10:GLU:N	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:j:154:CYS:C	40:j:156:THR:H	2.27	0.42
41:k:101:ARG:NH1	58:h:774:G:OP1	2.52	0.42
42:l:50:ALA:HA	42:l:56:LEU:HD12	2.02	0.42
48:r:76:TYR:HB2	53:w:72:THR:HG23	2.02	0.42
53:w:27:VAL:HG23	53:w:80:ILE:HG23	2.02	0.42
54:x:49:ASP:OD2	58:h:621:U:O2'	2.23	0.42
58:h:1476:G:H2'	58:h:1477:C:H6	1.83	0.42
58:h:2011:U:H2'	58:h:2012:C:H6	1.84	0.42
58:h:2147:U:H2'	58:h:2148:C:C6	2.55	0.42
58:h:2613:G:H5''	58:h:2614:U:O4'	2.20	0.42
5:7:286:ILE:HG23	5:7:290:PHE:CD2	2.55	0.42
5:7:326:LYS:HB3	5:7:338:LEU:HB2	2.02	0.42
5:7:701:SER:HB2	58:h:2884:A:H62	1.85	0.42
6:A:390:U:H4'	21:P:29:ARG:NH2	2.35	0.42
6:A:408:G:H4'	9:D:104:ARG:NH2	2.35	0.42
6:A:455:G:C2	6:A:459:G:C6	3.07	0.42
6:A:658:U:H2'	6:A:659:C:H6	1.84	0.42
7:B:46:A:C4	7:B:47:A:C8	3.08	0.42
14:I:126:ARG:NH1	14:I:127:ASP:O	2.53	0.42
15:J:7:ARG:C	15:J:8:ILE:HD13	2.45	0.42
16:K:118:THR:O	16:K:119:ILE:HD13	2.19	0.42
18:M:11:ARG:O	18:M:45:THR:HB	2.19	0.42
21:P:88:GLY:O	21:P:90:GLU:HG3	2.20	0.42
28:W:113:LEU:O	28:W:145:THR:HA	2.20	0.42
36:e:25:GLN:HE22	49:s:65:LYS:HG2	1.84	0.42
37:f:5:PRO:HD2	58:h:2689:C:O3'	2.20	0.42
39:i:206:TRP:O	39:i:211:ARG:HD3	2.20	0.42
46:p:55:VAL:HG13	46:p:79:LYS:HE2	2.02	0.42
51:u:102:ASN:ND2	51:u:107:ASN:OD1	2.34	0.42
58:h:419:G:C5	58:h:420:G:H1'	2.55	0.42
58:h:964:C:H2'	58:h:965:U:C6	2.55	0.42
58:h:1222:C:H2'	58:h:1223:U:C6	2.55	0.42
58:h:1436:C:HO2'	58:h:1437:A:P	2.43	0.42
58:h:1964:U:H2'	58:h:1965:G:H8	1.85	0.42
5:7:45:VAL:HA	5:7:50:LEU:O	2.20	0.41
6:A:581:U:H2'	6:A:582:U:C6	2.55	0.41
6:A:593:C:H2'	6:A:594:A:C8	2.53	0.41
6:A:1138:A:H62	6:A:1159:G:H21	1.67	0.41
11:F:18:THR:C	11:F:21:PRO:HD2	2.45	0.41
42:l:12:LYS:HG3	42:l:104:TRP:CD1	2.55	0.41
42:l:67:ILE:HA	42:l:147:GLU:OE1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:t:118:LEU:HD23	50:t:118:LEU:HA	1.83	0.41
55:y:30:GLU:H	55:y:30:GLU:HG3	1.67	0.41
58:h:289:A:C6	58:h:290:C:H5	2.38	0.41
58:h:718:C:O2'	58:h:772:U:OP1	2.35	0.41
58:h:1002:C:O2'	58:h:1003:A:OP1	2.24	0.41
58:h:1138:A:N1	58:h:1259:U:H2'	2.35	0.41
58:h:1904:C:H2'	58:h:1905:G:O4'	2.20	0.41
5:7:643:PRO:HB3	5:7:716:TYR:CE1	2.55	0.41
6:A:223:G:H2'	6:A:224:U:O4'	2.20	0.41
6:A:436:C:H2'	6:A:437:U:C6	2.55	0.41
6:A:877:G:H2'	6:A:878:C:C6	2.55	0.41
6:A:1020:G:H2'	6:A:1020:G:N3	2.36	0.41
6:A:1394:U:H2'	6:A:1395:C:H6	1.84	0.41
7:B:107:A:H2'	7:B:108:C:C6	2.55	0.41
8:C:30:ASP:HA	8:C:33:LYS:HG2	2.01	0.41
17:L:110:ARG:HE	17:L:110:ARG:HB2	1.73	0.41
18:M:59:TYR:CD1	18:M:59:TYR:C	2.97	0.41
18:M:90:LEU:HD23	18:M:90:LEU:HA	1.86	0.41
27:V:117:LEU:HD13	27:V:141:LYS:HG3	2.02	0.41
31:Z:48:ARG:NH2	58:h:58:G:OP1	2.54	0.41
40:j:37:THR:OG1	40:j:51:GLN:HG2	2.20	0.41
46:p:68:PHE:CZ	46:p:70:PHE:HB3	2.55	0.41
47:q:96:HIS:HA	47:q:97:PRO:HD3	1.86	0.41
50:t:47:ILE:HD12	50:t:70:PRO:HG3	2.01	0.41
58:h:217:G:N2	58:h:235:U:H4'	2.34	0.41
58:h:1186:G:N2	58:h:1213:A:HO2'	2.04	0.41
58:h:1187:A:C5	58:h:1191:A:H2	2.37	0.41
58:h:1287:C:H2'	58:h:1288:A:H8	1.85	0.41
58:h:1430:C:C2	58:h:1453:G:N2	2.88	0.41
58:h:1610:C:C2	58:h:1611:A:C8	3.08	0.41
58:h:1738:G:C2	58:h:1739:A:C8	3.08	0.41
5:7:326:LYS:HD3	5:7:338:LEU:HD23	2.01	0.41
5:7:353:HIS:HB2	5:7:430:LYS:HA	2.01	0.41
6:A:7:U:H5'	6:A:8:U:OP1	2.20	0.41
6:A:109:G:H2'	6:A:110:U:H6	1.86	0.41
6:A:209:A:H2'	6:A:210:A:C8	2.54	0.41
6:A:498:C:H4'	6:A:499:C:O5'	2.18	0.41
6:A:934:U:H2'	6:A:935:G:H8	1.85	0.41
6:A:1207:C:OP1	18:M:91:ARG:NH2	2.34	0.41
6:A:1297:U:H2'	6:A:1298:G:O4'	2.19	0.41
8:C:29:LYS:HE2	8:C:29:LYS:HB3	1.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:G:22:LEU:HD23	12:G:22:LEU:HA	1.77	0.41
12:G:57:ASP:OD1	12:G:58:PRO:HD2	2.20	0.41
25:T:2:ALA:HB1	25:T:8:ILE:HG12	2.02	0.41
28:W:33:VAL:N	28:W:49:LEU:O	2.46	0.41
41:k:61:GLY:HA3	41:k:80:ARG:HG2	2.02	0.41
43:m:22:GLN:HE21	43:m:39:GLU:HA	1.83	0.41
44:n:124:ILE:CG2	44:n:125:LYS:N	2.84	0.41
58:h:498:G:H8	58:h:498:G:H5''	1.85	0.41
5:7:232:SER:HA	5:7:262:ARG:HH12	1.86	0.41
5:7:575:PHE:CZ	5:7:613:SER:HA	2.55	0.41
5:7:674:ASP:HB2	5:7:682:VAL:HB	2.01	0.41
6:A:522:G:C5'	9:D:10:ARG:HH22	2.34	0.41
6:A:1273:C:OP1	12:G:37:SER:OG	2.30	0.41
6:A:1297:U:O2'	6:A:1342:A:N3	2.45	0.41
6:A:1342:A:OP2	19:N:35:ARG:NH2	2.54	0.41
8:C:189:ALA:N	8:C:196:ILE:O	2.45	0.41
11:F:48:LEU:HD13	11:F:52:ILE:HG22	2.01	0.41
15:J:8:ILE:HB	15:J:74:ILE:HB	2.01	0.41
22:Q:23:ALA:O	22:Q:24:ILE:HD13	2.20	0.41
27:V:99:GLY:O	27:V:103:ASN:HB3	2.20	0.41
27:V:216:VAL:O	27:V:219:SER:OG	2.37	0.41
28:W:102:ARG:HG3	28:W:138:LEU:HD12	2.02	0.41
54:x:11:GLN:O	54:x:15:ARG:HG3	2.20	0.41
58:h:1048:A:C6	58:h:1050:A:C8	3.09	0.41
58:h:1210:C:H2'	58:h:1211:G:C8	2.55	0.41
4:5:81:VAL:HG23	4:5:120:LEU:HD21	2.01	0.41
6:A:39:G:H2'	6:A:40:C:H6	1.81	0.41
6:A:969:G:H2'	6:A:970:G:H8	1.85	0.41
6:A:1287:G:H22	6:A:1313:G:H1'	1.85	0.41
7:B:30:G:H21	7:B:59:A:N6	2.18	0.41
12:G:105:VAL:O	12:G:109:ARG:HG3	2.20	0.41
14:I:58:TYR:HD1	14:I:59:PHE:CD1	2.37	0.41
18:M:78:ILE:O	18:M:82:ILE:HG22	2.20	0.41
20:O:7:GLN:H	20:O:7:GLN:CD	2.19	0.41
22:Q:41:GLU:OE2	22:Q:54:ARG:NH2	2.38	0.41
25:T:35:PHE:CD2	25:T:79:LEU:HD13	2.56	0.41
40:j:3:ARG:CZ	40:j:212:ILE:HG12	2.50	0.41
48:r:93:PRO:HG3	48:r:114:ILE:HD12	2.02	0.41
58:h:1035:G:H21	58:h:2493:A:H8	1.67	0.41
58:h:1781:C:H2'	58:h:1782:U:C6	2.55	0.41
58:h:2289:C:H2'	58:h:2290:C:H6	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:h:2466:G:H2'	58:h:2467:U:O4'	2.20	0.41
1:2:63:G:H2'	1:2:64:A:H8	1.86	0.41
6:A:421:U:H3'	6:A:422:C:H5'	2.02	0.41
6:A:452:A:O2'	21:P:76:ILE:HD11	2.21	0.41
6:A:965:A:H5'	6:A:966:C:OP2	2.21	0.41
7:B:102:A:H2'	7:B:103:G:O4'	2.20	0.41
8:C:129:PHE:HD1	8:C:133:MET:HE3	1.85	0.41
11:F:74:GLU:O	11:F:78:GLN:HG2	2.20	0.41
15:J:57:LYS:HG3	15:J:58:TYR:N	2.35	0.41
17:L:94:ARG:HB2	17:L:95:TYR:CE1	2.56	0.41
21:P:84:LYS:HA	21:P:84:LYS:HD3	1.62	0.41
27:V:120:MET:HE2	27:V:120:MET:HB3	1.89	0.41
40:j:108:ASP:N	40:j:108:ASP:OD1	2.52	0.41
51:u:47:TYR:OH	51:u:69:LYS:HD2	2.21	0.41
58:h:980:C:HO2'	58:h:981:U:P	2.44	0.41
58:h:2090:U:O2	58:h:2093:G:C2	2.74	0.41
58:h:2761:U:H2'	58:h:2762:C:H6	1.84	0.41
4:5:62:GLU:HA	4:5:107:LYS:HA	2.03	0.41
5:7:423:THR:HG22	5:7:439:TRP:HH2	1.85	0.41
5:7:439:TRP:H	5:7:439:TRP:HE3	1.66	0.41
6:A:92:A:O2'	6:A:93:C:H6	2.04	0.41
6:A:194:A:H61	22:Q:20:ARG:HH12	1.67	0.41
6:A:580:G:H2'	6:A:581:U:C6	2.56	0.41
6:A:940:A:C6	24:S:55:ARG:HB2	2.56	0.41
6:A:985:G:H1	6:A:1018:C:H42	1.68	0.41
6:A:1100:U:H2'	6:A:1101:C:H6	1.86	0.41
6:A:1229:A:H4'	14:I:53:ARG:NH1	2.33	0.41
6:A:1269:A:H2'	6:A:1270:A:C8	2.56	0.41
6:A:1429:A:O2'	6:A:1430:A:H5'	2.20	0.41
11:F:46:ARG:HB2	11:F:60:TYR:CE2	2.56	0.41
11:F:50:TYR:OH	11:F:87:ARG:NH1	2.54	0.41
14:I:147:TYR:OH	14:I:149:LYS:HB3	2.20	0.41
17:L:33:VAL:O	17:L:56:LYS:N	2.46	0.41
23:R:56:ASN:OD1	23:R:56:ASN:N	2.48	0.41
39:i:133:LEU:HB2	39:i:189:CYS:O	2.20	0.41
39:i:162:SER:HB3	39:i:195:GLU:HG3	2.02	0.41
40:j:104:GLU:H	40:j:104:GLU:HG2	1.63	0.41
46:p:70:PHE:HD2	46:p:72:LEU:HG	1.84	0.41
58:h:81:A:C2	58:h:100:A:C5	3.08	0.41
58:h:1185:A:O2'	58:h:1186:G:O4'	2.39	0.41
58:h:2042:A:H2'	58:h:2043:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:h:2374:U:H2'	58:h:2375:G:H8	1.85	0.41
58:h:2736:C:H2'	58:h:2737:G:O4'	2.21	0.41
58:h:2807:G:H2'	58:h:2808:U:O4'	2.20	0.41
58:h:3057:U:H2'	58:h:3058:A:C8	2.56	0.41
1:2:34:C:H5'	6:A:948:G:C2	2.55	0.41
1:2:56:C:O4'	42:l:80:SER:HB3	2.21	0.41
4:5:74:LYS:NZ	4:5:97:VAL:HG13	2.35	0.41
5:7:210:ASP:N	5:7:210:ASP:OD1	2.52	0.41
5:7:336:VAL:HA	5:7:416:GLY:HA2	2.02	0.41
5:7:441:MET:HE3	5:7:441:MET:C	2.46	0.41
6:A:1105:U:HO2'	6:A:1106:U:P	2.43	0.41
6:A:1306:A:H2'	6:A:1307:C:H6	1.85	0.41
6:A:1491:A:H2'	6:A:1492:G:C8	2.55	0.41
40:j:27:THR:OG1	40:j:196:GLY:O	2.38	0.41
42:l:141:GLU:HG3	42:l:142:GLN:N	2.35	0.41
43:m:76:LEU:HA	43:m:76:LEU:HD12	1.86	0.41
58:h:395:G:H2'	58:h:396:C:C6	2.56	0.41
58:h:563:U:H4'	58:h:597:C:H5'	2.03	0.41
58:h:844:G:H4'	58:h:878:G:H5'	2.01	0.41
58:h:1556:A:N1	58:h:1615:G:C6	2.88	0.41
58:h:1854:U:H2'	58:h:1855:A:H8	1.86	0.41
58:h:2011:U:H2'	58:h:2012:C:C6	2.56	0.41
58:h:3118:U:H2'	58:h:3119:A:C8	2.55	0.41
5:7:392:THR:HG23	5:7:417:ARG:NE	2.36	0.41
6:A:200:U:H6	6:A:200:U:H2'	1.72	0.41
6:A:323:U:O3'	25:T:17:ARG:HG2	2.21	0.41
6:A:561:G:OP1	20:O:65:ARG:NH2	2.53	0.41
6:A:594:A:H2'	6:A:595:C:H6	1.86	0.41
6:A:664:U:O2	16:K:50:VAL:HG12	2.21	0.41
6:A:993:G:H2'	6:A:994:C:H6	1.85	0.41
6:A:1082:A:H2'	6:A:1083:C:C6	2.56	0.41
6:A:1087:C:C4	6:A:1088:G:C8	3.08	0.41
6:A:1264:C:C4	6:A:1265:U:C4	3.09	0.41
8:C:20:SER:HB3	8:C:39:ARG:NH2	2.36	0.41
9:D:23:ASP:OD1	9:D:23:ASP:C	2.64	0.41
11:F:44:GLY:O	11:F:46:ARG:NH1	2.54	0.41
11:F:83:GLU:N	11:F:83:GLU:OE1	2.53	0.41
12:G:44:TYR:O	12:G:48:GLU:HG2	2.21	0.41
13:H:52:GLU:HG2	13:H:53:ASP:N	2.35	0.41
18:M:48:LEU:HD12	18:M:49:THR:H	1.85	0.41
21:P:92:THR:HG22	21:P:92:THR:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:Q:77:MET:HG3	22:Q:91:VAL:HG11	2.02	0.41
27:V:27:MET:SD	27:V:193:PRO:HD3	2.61	0.41
27:V:45:GLN:O	27:V:49:TYR:HD2	2.04	0.41
33:b:42:ARG:HB3	33:b:43:LEU:HD12	2.03	0.41
34:c:11:ILE:HD12	34:c:13:LEU:HD21	2.01	0.41
40:j:28:VAL:HG22	40:j:193:LEU:HD22	2.03	0.41
41:k:28:GLU:N	41:k:28:GLU:OE1	2.51	0.41
42:l:58:ASN:O	42:l:61:ILE:HG12	2.21	0.41
45:o:123:ILE:HA	45:o:126:LEU:HD12	2.02	0.41
46:p:38:MET:H	46:p:38:MET:HG2	1.74	0.41
46:p:75:PRO:HA	46:p:76:PRO:HD3	1.97	0.41
49:s:80:VAL:HG22	49:s:114:GLY:HA2	2.02	0.41
55:y:53:ASP:O	55:y:57:LYS:HG2	2.21	0.41
57:1:77:ASP:OD1	57:1:77:ASP:N	2.54	0.41
58:h:194:A:H61	58:h:197:C:H3'	1.84	0.41
58:h:678:A:N1	58:h:924:G:O2'	2.39	0.41
58:h:784:G:H2'	58:h:784:G:N3	2.36	0.41
58:h:859:G:H2'	58:h:860:G:O4'	2.21	0.41
58:h:929:C:H2'	58:h:930:C:C6	2.56	0.41
58:h:1177:G:P	58:h:1178:U:H3'	2.61	0.41
58:h:1552:A:H2'	58:h:1617:C:N4	2.35	0.41
58:h:2413:G:C2	58:h:2414:G:C8	3.09	0.41
58:h:2691:C:H2'	58:h:2692:A:O4'	2.20	0.41
5:7:353:HIS:O	5:7:427:LEU:HA	2.21	0.41
5:7:619:PHE:CZ	6:A:1477:A:H2	2.39	0.41
6:A:1089:C:C2	6:A:1090:A:C8	3.08	0.41
6:A:1264:C:H2'	6:A:1265:U:C6	2.56	0.41
10:E:43:ILE:HD12	10:E:81:VAL:HG13	2.03	0.41
12:G:111:ARG:HB3	12:G:119:ARG:HD2	2.03	0.41
15:J:7:ARG:HH21	15:J:73:LEU:HD21	1.85	0.41
17:L:5:GLN:HB2	22:Q:51:LYS:NZ	2.36	0.41
17:L:7:LEU:HD23	22:Q:49:TYR:CE1	2.56	0.41
18:M:7:VAL:HG12	18:M:9:LEU:HD23	2.03	0.41
22:Q:43:ARG:HH11	22:Q:43:ARG:HG2	1.86	0.41
26:U:62:ARG:NH1	58:h:1454:G:N7	2.69	0.41
31:Z:5:THR:HG21	31:Z:21:LYS:HE3	2.03	0.41
39:i:155:LEU:HG	39:i:177:MET:HE1	2.03	0.41
43:m:5:GLY:HA3	43:m:66:HIS:ND1	2.36	0.41
50:t:42:ILE:HD12	50:t:97:VAL:HG21	2.02	0.41
56:z:77:VAL:HG21	56:z:117:ARG:HH11	1.86	0.41
58:h:750:C:H2'	58:h:751:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:h:1002:C:C2'	58:h:1003:A:H5''	2.51	0.41
58:h:1489:G:H2'	58:h:1490:U:O4'	2.21	0.41
58:h:1651:C:H2'	58:h:1652:A:C8	2.55	0.41
58:h:1651:C:H2'	58:h:1652:A:H8	1.85	0.41
58:h:2086:U:H2'	58:h:2087:C:C6	2.56	0.41
58:h:2142:A:O2'	58:h:2144:C:N4	2.54	0.41
58:h:2323:G:N2	58:h:2412:U:O2	2.44	0.41
58:h:2465:A:H2'	58:h:2466:G:C8	2.56	0.41
58:h:2505:C:O2'	58:h:2506:G:H5'	2.21	0.41
5:7:309:ARG:NH2	5:7:312:LEU:HG	2.36	0.40
5:7:447:PRO:HA	5:7:489:TRP:HA	2.03	0.40
6:A:160:C:H2'	6:A:161:U:O4'	2.22	0.40
6:A:572:G:H2'	6:A:573:U:C6	2.56	0.40
6:A:749:G:H4'	6:A:1497:A:H4'	2.02	0.40
6:A:830:G:H2'	6:A:831:A:H8	1.85	0.40
18:M:33:ILE:HG12	18:M:59:TYR:CE1	2.56	0.40
23:R:70:ASN:O	23:R:74:VAL:HG22	2.21	0.40
26:U:38:ASN:O	26:U:42:ILE:HG13	2.21	0.40
43:m:42:SER:OG	43:m:54:THR:HB	2.22	0.40
44:n:41:ARG:HH11	58:h:306:U:H5''	1.86	0.40
58:h:790:A:N3	58:h:2667:C:O2'	2.51	0.40
58:h:3115:A:H2'	58:h:3116:C:C6	2.56	0.40
5:7:208:PRO:HA	5:7:209:PRO:HD3	1.91	0.40
5:7:520:LEU:HG	5:7:521:ARG:N	2.36	0.40
6:A:315:A:N7	6:A:328:U:H5	2.20	0.40
6:A:494:C:H2'	6:A:495:G:H8	1.86	0.40
6:A:1266:U:C4	6:A:1267:U:H5	2.40	0.40
10:E:191:PRO:O	10:E:195:LEU:HG	2.22	0.40
11:F:12:PRO:O	11:F:45:ARG:NH1	2.54	0.40
11:F:77:ARG:NH1	39:i:126:LYS:HE3	2.36	0.40
39:i:227:ASN:OD1	58:h:899:G:H5'	2.20	0.40
43:m:9:VAL:HG22	43:m:51:ILE:HB	2.02	0.40
47:q:13:ARG:CZ	47:q:121:LYS:HE2	2.51	0.40
48:r:113:LYS:HA	48:r:113:LYS:HD2	1.80	0.40
57:1:4:HIS:NE2	58:h:81:A:OP1	2.53	0.40
58:h:247:G:H4'	58:h:474:G:C5	2.57	0.40
58:h:908:A:OP2	58:h:2294:A:O2'	2.38	0.40
58:h:922:U:O2'	58:h:2284:A:N1	2.50	0.40
58:h:979:G:H2'	58:h:980:C:H6	1.86	0.40
58:h:1224:G:N3	58:h:1225:G:C8	2.89	0.40
58:h:2323:G:H2'	58:h:2324:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:h:2394:A:O2'	58:h:2395:U:H5'	2.21	0.40
6:A:440:C:C2	6:A:441:A:C8	3.10	0.40
6:A:748:A:H4'	6:A:1507:G:N2	2.36	0.40
6:A:1153:U:H2'	6:A:1154:C:H6	1.84	0.40
6:A:1483:A:H1'	6:A:1504:G:H5'	2.02	0.40
11:F:36:THR:HB	11:F:66:LYS:O	2.21	0.40
18:M:39:ILE:HD13	18:M:52:GLN:HB3	2.02	0.40
18:M:117:ILE:HD13	18:M:117:ILE:HA	1.89	0.40
27:V:134:ILE:HD13	27:V:134:ILE:HA	1.85	0.40
34:c:19:LYS:HE3	34:c:19:LYS:HB3	1.86	0.40
36:e:30:ARG:HA	36:e:30:ARG:HD2	1.85	0.40
38:g:24:THR:OG1	38:g:25:ARG:N	2.54	0.40
42:l:70:GLN:HE21	42:l:102:ARG:HD3	1.86	0.40
42:l:72:PRO:HB2	42:l:94:ALA:HB1	2.03	0.40
43:m:61:ARG:CZ	43:m:61:ARG:HB3	2.51	0.40
45:o:6:LYS:NZ	58:h:1164:A:O3'	2.53	0.40
45:o:16:GLN:HB3	45:o:81:PHE:CE2	2.57	0.40
49:s:77:VAL:HA	49:s:111:LYS:O	2.21	0.40
58:h:278:A:H2'	58:h:279:U:C6	2.57	0.40
58:h:579:A:H2'	58:h:580:G:O4'	2.21	0.40
58:h:735:U:H2'	58:h:736:G:O4'	2.21	0.40
58:h:864:A:C2	58:h:865:A:C8	3.09	0.40
58:h:1086:C:H4'	58:h:1086:C:OP2	2.22	0.40
58:h:1610:C:C4	58:h:1611:A:N7	2.89	0.40
58:h:3030:A:H2'	58:h:3031:A:C8	2.56	0.40
3:4:7:G:H2'	3:4:8:A:C8	2.56	0.40
6:A:36:A:H2'	6:A:37:A:C8	2.57	0.40
6:A:229:U:O2'	21:P:24:ASP:OD1	2.39	0.40
6:A:253:U:O2'	22:Q:32:MET:HE1	2.21	0.40
6:A:1118:A:OP1	6:A:1118:A:C8	2.75	0.40
6:A:1141:G:C2	6:A:1142:C:C6	3.09	0.40
7:B:28:A:H5'	52:v:46:HIS:CD2	2.57	0.40
8:C:90:LEU:HD13	8:C:98:VAL:HG11	2.02	0.40
9:D:92:ARG:HH12	9:D:129:SER:HB2	1.86	0.40
12:G:135:VAL:O	12:G:139:GLU:HG2	2.21	0.40
21:P:7:LEU:HB3	21:P:18:TYR:HD2	1.86	0.40
39:i:208:LYS:HB2	58:h:844:G:C5	2.56	0.40
41:k:2:THR:HB	41:k:19:GLU:OE1	2.21	0.40
41:k:139:LYS:HE2	58:h:402:G:N7	2.36	0.40
58:h:159:A:N3	58:h:2431:C:O2'	2.46	0.40
58:h:1557:C:H2'	58:h:1558:C:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:h:2363:A:H61	58:h:2374:U:H3	1.68	0.40
58:h:2603:G:H2'	58:h:2604:U:C6	2.56	0.40
1:2:30:G:OP1	6:A:1210:A:O2'	2.36	0.40
6:A:270:A:H2'	6:A:271:C:C6	2.57	0.40
6:A:525:C:O2'	6:A:529:C:OP1	2.37	0.40
6:A:829:G:C2	6:A:830:G:C8	3.10	0.40
6:A:1066:U:C2	6:A:1067:G:C8	3.10	0.40
6:A:1094:C:H2'	6:A:1095:U:H6	1.86	0.40
6:A:1207:C:N4	18:M:104:LYS:HD2	2.35	0.40
6:A:1434:U:O2'	6:A:1435:U:H5''	2.21	0.40
11:F:43:TRP:HB2	11:F:46:ARG:NH2	2.37	0.40
12:G:90:GLU:H	12:G:90:GLU:HG3	1.75	0.40
13:H:41:LYS:NZ	13:H:47:SER:O	2.55	0.40
15:J:4:GLN:O	15:J:79:PRO:HD3	2.21	0.40
17:L:43:LYS:HE3	17:L:43:LYS:HA	2.02	0.40
32:a:18:LYS:O	32:a:22:SER:OG	2.27	0.40
32:a:38:GLU:HG3	32:a:39:ASP:H	1.86	0.40
43:m:23:ASN:OD1	43:m:23:ASN:C	2.64	0.40
48:r:24:VAL:HG13	48:r:33:ALA:HB2	2.04	0.40
49:s:106:LYS:H	49:s:106:LYS:HG2	1.70	0.40
56:z:18:ARG:NH1	56:z:18:ARG:HG2	2.35	0.40
57:1:93:LYS:HE3	57:1:93:LYS:HB3	1.79	0.40
58:h:257:A:H2'	58:h:258:G:O4'	2.22	0.40
58:h:321:G:H2'	58:h:322:A:C8	2.56	0.40
58:h:750:C:H2'	58:h:751:A:H8	1.87	0.40
58:h:1081:C:O2'	58:h:2497:A:N3	2.48	0.40
58:h:1118:A:H2'	58:h:1119:A:C8	2.57	0.40
58:h:1225:G:C5	58:h:1226:U:C4	3.09	0.40
58:h:1437:A:C5	58:h:1438:G:N7	2.89	0.40
58:h:1621:C:H2'	58:h:1622:G:H8	1.86	0.40
58:h:1964:U:H2'	58:h:1965:G:C8	2.56	0.40
58:h:2147:U:H2'	58:h:2148:C:H6	1.86	0.40
58:h:2365:A:H2'	58:h:2366:C:H6	1.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	3	21/23 (91%)	20 (95%)	1 (5%)	0	100	100
4	5	67/69 (97%)	61 (91%)	4 (6%)	2 (3%)	3	22
5	7	707/709 (100%)	673 (95%)	33 (5%)	1 (0%)	48	83
8	C	206/208 (99%)	192 (93%)	14 (7%)	0	100	100
9	D	198/200 (99%)	186 (94%)	12 (6%)	0	100	100
10	E	178/180 (99%)	168 (94%)	10 (6%)	0	100	100
11	F	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
12	G	153/155 (99%)	149 (97%)	4 (3%)	0	100	100
13	H	129/131 (98%)	127 (98%)	2 (2%)	0	100	100
14	I	124/126 (98%)	116 (94%)	8 (6%)	0	100	100
15	J	97/99 (98%)	92 (95%)	4 (4%)	1 (1%)	12	47
16	K	113/115 (98%)	110 (97%)	3 (3%)	0	100	100
17	L	120/122 (98%)	111 (92%)	9 (8%)	0	100	100
18	M	114/116 (98%)	107 (94%)	7 (6%)	0	100	100
19	N	58/60 (97%)	50 (86%)	8 (14%)	0	100	100
20	O	86/88 (98%)	85 (99%)	1 (1%)	0	100	100
21	P	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
22	Q	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
23	R	63/65 (97%)	61 (97%)	2 (3%)	0	100	100
24	S	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
25	T	83/85 (98%)	81 (98%)	2 (2%)	0	100	100
26	U	95/97 (98%)	92 (97%)	3 (3%)	0	100	100
27	V	226/228 (99%)	215 (95%)	10 (4%)	1 (0%)	30	67
28	W	190/192 (99%)	183 (96%)	7 (4%)	0	100	100
29	X	77/79 (98%)	71 (92%)	6 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	Y	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
31	Z	62/64 (97%)	61 (98%)	1 (2%)	0	100	100
32	a	57/59 (97%)	56 (98%)	1 (2%)	0	100	100
33	b	52/54 (96%)	50 (96%)	2 (4%)	0	100	100
34	c	47/49 (96%)	45 (96%)	1 (2%)	1 (2%)	5	29
35	d	44/46 (96%)	44 (100%)	0	0	100	100
36	e	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
37	f	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
38	g	46/48 (96%)	43 (94%)	3 (6%)	0	100	100
39	i	273/275 (99%)	261 (96%)	12 (4%)	0	100	100
40	j	212/214 (99%)	200 (94%)	12 (6%)	0	100	100
41	k	207/209 (99%)	201 (97%)	6 (3%)	0	100	100
42	l	180/182 (99%)	170 (94%)	10 (6%)	0	100	100
43	m	174/176 (99%)	169 (97%)	5 (3%)	0	100	100
44	n	149/151 (99%)	138 (93%)	11 (7%)	0	100	100
45	o	124/126 (98%)	118 (95%)	6 (5%)	0	100	100
46	p	131/133 (98%)	123 (94%)	6 (5%)	2 (2%)	8	38
47	q	144/146 (99%)	141 (98%)	3 (2%)	0	100	100
48	r	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
49	s	143/145 (99%)	126 (88%)	17 (12%)	0	100	100
50	t	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
51	u	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
52	v	124/126 (98%)	123 (99%)	1 (1%)	0	100	100
53	w	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
54	x	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
55	y	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
56	z	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
57	1	93/105 (89%)	92 (99%)	1 (1%)	0	100	100
All	All	6714/6830 (98%)	6408 (95%)	298 (4%)	8 (0%)	49	83

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	5	99	SER
34	c	7	VAL
27	V	155	GLN
5	7	677	ASP
15	J	57	LYS
4	5	100	ALA
46	p	24	PRO
46	p	25	PRO

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	3	18/18 (100%)	18 (100%)	0	100	100
4	5	53/53 (100%)	53 (100%)	0	100	100
5	7	564/564 (100%)	557 (99%)	7 (1%)	63	74
8	C	170/170 (100%)	169 (99%)	1 (1%)	78	81
9	D	175/175 (100%)	174 (99%)	1 (1%)	78	81
10	E	127/127 (100%)	125 (98%)	2 (2%)	55	69
11	F	85/85 (100%)	82 (96%)	3 (4%)	32	54
12	G	131/131 (100%)	130 (99%)	1 (1%)	73	78
13	H	107/107 (100%)	107 (100%)	0	100	100
14	I	102/102 (100%)	100 (98%)	2 (2%)	48	66
15	J	89/89 (100%)	87 (98%)	2 (2%)	45	64
16	K	89/89 (100%)	87 (98%)	2 (2%)	45	64
17	L	103/103 (100%)	103 (100%)	0	100	100
18	M	99/99 (100%)	99 (100%)	0	100	100
19	N	49/49 (100%)	49 (100%)	0	100	100
20	O	76/76 (100%)	76 (100%)	0	100	100
21	P	92/92 (100%)	92 (100%)	0	100	100
22	Q	80/80 (100%)	80 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	R	55/55 (100%)	54 (98%)	1 (2%)	51	67
24	S	73/73 (100%)	70 (96%)	3 (4%)	27	49
25	T	69/69 (100%)	67 (97%)	2 (3%)	37	58
26	U	83/83 (100%)	82 (99%)	1 (1%)	63	74
27	V	191/191 (100%)	190 (100%)	1 (0%)	81	82
28	W	155/155 (100%)	155 (100%)	0	100	100
29	X	58/58 (100%)	58 (100%)	0	100	100
30	Y	50/50 (100%)	50 (100%)	0	100	100
31	Z	58/58 (100%)	58 (100%)	0	100	100
32	a	52/52 (100%)	51 (98%)	1 (2%)	50	66
33	b	43/43 (100%)	43 (100%)	0	100	100
34	c	47/47 (100%)	47 (100%)	0	100	100
35	d	35/35 (100%)	35 (100%)	0	100	100
36	e	53/53 (100%)	53 (100%)	0	100	100
37	f	35/35 (100%)	35 (100%)	0	100	100
38	g	43/43 (100%)	43 (100%)	0	100	100
39	i	215/215 (100%)	213 (99%)	2 (1%)	70	77
40	j	160/160 (100%)	156 (98%)	4 (2%)	42	62
41	k	169/169 (100%)	168 (99%)	1 (1%)	78	81
42	l	151/151 (100%)	148 (98%)	3 (2%)	48	66
43	m	148/148 (100%)	148 (100%)	0	100	100
44	n	90/116 (78%)	90 (100%)	0	100	100
45	o	89/89 (100%)	89 (100%)	0	100	100
46	p	102/102 (100%)	102 (100%)	0	100	100
47	q	119/119 (100%)	116 (98%)	3 (2%)	42	62
48	r	100/100 (100%)	99 (99%)	1 (1%)	68	76
49	s	112/112 (100%)	112 (100%)	0	100	100
50	t	114/114 (100%)	112 (98%)	2 (2%)	51	67
51	u	97/97 (100%)	97 (100%)	0	100	100
52	v	93/93 (100%)	92 (99%)	1 (1%)	65	74
53	w	100/100 (100%)	100 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	x	97/97 (100%)	97 (100%)	0	100	100
55	y	81/81 (100%)	79 (98%)	2 (2%)	42	62
56	z	90/90 (100%)	90 (100%)	0	100	100
57	1	81/86 (94%)	81 (100%)	0	100	100
All	All	5517/5548 (99%)	5468 (99%)	49 (1%)	68	77

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	7	301	VAL
5	7	518	VAL
5	7	520	LEU
5	7	521	ARG
5	7	637	LYS
5	7	638	ILE
5	7	682	VAL
8	C	145	ASN
9	D	85	LEU
10	E	95	ASN
10	E	120	MET
11	F	15	ASP
11	F	41	ASP
11	F	52	ILE
12	G	94	ASP
14	I	110	VAL
14	I	147	TYR
15	J	82	LYS
15	J	87	LEU
16	K	128	ASN
16	K	137	ARG
23	R	31	ASP
24	S	12	ASP
24	S	14	HIS
24	S	48	THR
25	T	16	ARG
25	T	79	LEU
26	U	20	SER
27	V	41	ILE
32	a	58	GLU
39	i	163	ILE
39	i	270	ARG

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Mol	Chain	Res	Type
40	j	104	GLU
40	j	151	ILE
40	j	173	ASP
40	j	205	LEU
41	k	13	LYS
42	l	107	LEU
42	l	120	ASP
42	l	136	THR
47	q	69	LEU
47	q	96	HIS
47	q	108	MET
48	r	47	ILE
50	t	27	VAL
50	t	31	ASP
52	v	25	LEU
55	y	54	ASP
55	y	73	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
2	3	23	ASN
5	7	586	GLN
5	7	612	HIS
5	7	639	ASN
8	C	125	ASN
9	D	48	GLN
9	D	173	GLN
12	G	86	GLN
18	M	101	GLN
19	N	49	HIS
24	S	26	ASN
24	S	29	GLN
27	V	45	GLN
28	W	180	ASN
31	Z	31	ASN
31	Z	44	ASN
32	a	8	GLN
32	a	42	GLN
33	b	12	ASN
36	e	25	GLN
39	i	96	HIS

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Mol	Chain	Res	Type
40	j	21	ASN
40	j	76	ASN
40	j	130	HIS
41	k	91	HIS
41	k	202	ASN
42	l	70	GLN
43	m	98	GLN
47	q	58	ASN
49	s	69	ASN
50	t	9	HIS
51	u	62	ASN
52	v	16	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	75/76 (98%)	16 (21%)	0
3	4	17/18 (94%)	4 (23%)	1 (5%)
58	h	3069/3127 (98%)	563 (18%)	0
6	A	1510/1511 (99%)	299 (19%)	11 (0%)
7	B	117/118 (99%)	17 (14%)	1 (0%)
All	All	4788/4850 (98%)	899 (18%)	13 (0%)

All (899) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	16	U
1	2	17	C
1	2	19	G
1	2	20	U
1	2	21	A
1	2	22	G
1	2	23	A
1	2	42	C
1	2	43	C
1	2	46	G
1	2	47	U
1	2	48	C
1	2	52	G
1	2	69	G
1	2	70	G

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Mol	Chain	Res	Type
1	2	76	A
3	4	12	A
3	4	13	A
3	4	19	C
3	4	20	C
6	A	8	U
6	A	9	U
6	A	11	G
6	A	12	A
6	A	13	G
6	A	36	A
6	A	43	G
6	A	52	U
6	A	53	U
6	A	54	A
6	A	55	A
6	A	58	C
6	A	59	A
6	A	77	G
6	A	82	U
6	A	83	U
6	A	85	C
6	A	87	G
6	A	89	G
6	A	93	C
6	A	116	A
6	A	117	C
6	A	118	A
6	A	126	G
6	A	128	U
6	A	139	C
6	A	160	C
6	A	170	U
6	A	179	C
6	A	180	A
6	A	192	G
6	A	193	C
6	A	201	G
6	A	210	A
6	A	211	A
6	A	215	U
6	A	217	U

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Mol	Chain	Res	Type
6	A	218	G
6	A	243	A
6	A	244	U
6	A	245	C
6	A	247	G
6	A	251	G
6	A	266	G
6	A	267	C
6	A	279	A
6	A	280	C
6	A	281	G
6	A	289	G
6	A	321	A
6	A	328	U
6	A	329	A
6	A	332	G
6	A	344	A
6	A	345	C
6	A	347	G
6	A	351	G
6	A	352	C
6	A	353	A
6	A	354	G
6	A	356	A
6	A	367	U
6	A	371	A
6	A	372	C
6	A	373	A
6	A	388	G
6	A	390	U
6	A	397	A
6	A	398	C
6	A	406	G
6	A	412	U
6	A	413	G
6	A	414	A
6	A	419	C
6	A	421	U
6	A	422	C
6	A	423	G
6	A	424	G
6	A	429	U

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Mol	Chain	Res	Type
6	A	430	A
6	A	433	C
6	A	434	C
6	A	438	U
6	A	451	A
6	A	452	A
6	A	453	G
6	A	454	C
6	A	456	C
6	A	457	A
6	A	458	A
6	A	459	G
6	A	461	G
6	A	464	G
6	A	465	G
6	A	466	U
6	A	476	A
6	A	477	G
6	A	478	A
6	A	482	A
6	A	485	G
6	A	486	G
6	A	488	C
6	A	490	A
6	A	491	C
6	A	497	G
6	A	498	C
6	A	499	C
6	A	505	C
6	A	507	G
6	A	509	G
6	A	511	U
6	A	512	A
6	A	513	A
6	A	515	A
6	A	520	G
6	A	525	C
6	A	527	A
6	A	539	A
6	A	542	U
6	A	544	C
6	A	552	A

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Mol	Chain	Res	Type
6	A	553	A
6	A	556	A
6	A	557	G
6	A	576	C
6	A	612	U
6	A	613	G
6	A	633	A
6	A	645	G
6	A	666	U
6	A	668	G
6	A	680	G
6	A	683	G
6	A	700	C
6	A	701	G
6	A	702	G
6	A	703	U
6	A	711	G
6	A	728	A
6	A	729	A
6	A	735	G
6	A	757	A
6	A	761	A
6	A	765	G
6	A	772	A
6	A	773	U
6	A	774	A
6	A	789	G
6	A	795	A
6	A	797	C
6	A	799	G
6	A	808	A
6	A	821	C
6	A	822	U
6	A	823	U
6	A	824	C
6	A	826	U
6	A	827	U
6	A	828	G
6	A	841	U
6	A	864	C
6	A	865	C
6	A	884	G

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Mol	Chain	Res	Type
6	A	896	A
6	A	908	G
6	A	909	G
6	A	914	C
6	A	916	C
6	A	921	G
6	A	942	U
6	A	943	U
6	A	948	G
6	A	950	A
6	A	951	A
6	A	953	G
6	A	955	G
6	A	956	A
6	A	957	A
6	A	958	G
6	A	959	A
6	A	971	G
6	A	973	U
6	A	974	U
6	A	975	G
6	A	976	A
6	A	982	A
6	A	985	G
6	A	986	G
6	A	987	A
6	A	988	C
6	A	1003	C
6	A	1007	U
6	A	1008	C
6	A	1010	C
6	A	1013	G
6	A	1014	U
6	A	1020	G
6	A	1024	G
6	A	1025	C
6	A	1028	G
6	A	1033	G
6	A	1034	C
6	A	1036	U
6	A	1045	U
6	A	1048	G

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Mol	Chain	Res	Type
6	A	1074	G
6	A	1075	U
6	A	1081	A
6	A	1104	G
6	A	1108	C
6	A	1110	A
6	A	1112	C
6	A	1115	G
6	A	1116	U
6	A	1117	U
6	A	1118	A
6	A	1120	G
6	A	1121	G
6	A	1123	G
6	A	1128	C
6	A	1129	U
6	A	1138	A
6	A	1140	U
6	A	1147	G
6	A	1149	C
6	A	1150	A
6	A	1162	G
6	A	1164	U
6	A	1165	G
6	A	1172	A
6	A	1177	A
6	A	1178	A
6	A	1181	C
6	A	1182	A
6	A	1193	U
6	A	1194	A
6	A	1206	U
6	A	1217	A
6	A	1219	A
6	A	1231	A
6	A	1234	G
6	A	1238	U
6	A	1241	G
6	A	1249	G
6	A	1251	G
6	A	1261	A
6	A	1266	U

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Mol	Chain	Res	Type
6	A	1267	U
6	A	1268	C
6	A	1272	G
6	A	1281	A
6	A	1282	G
6	A	1283	U
6	A	1284	U
6	A	1285	C
6	A	1287	G
6	A	1302	C
6	A	1313	G
6	A	1328	A
6	A	1329	G
6	A	1333	U
6	A	1335	G
6	A	1343	G
6	A	1344	C
6	A	1345	A
6	A	1346	A
6	A	1347	C
6	A	1351	G
6	A	1353	G
6	A	1356	G
6	A	1357	A
6	A	1364	U
6	A	1380	C
6	A	1381	A
6	A	1382	C
6	A	1389	U
6	A	1395	C
6	A	1405	G
6	A	1407	U
6	A	1425	G
6	A	1429	A
6	A	1434	U
6	A	1435	U
6	A	1436	G
6	A	1438	G
6	A	1459	G
6	A	1463	G
6	A	1466	G
6	A	1471	G

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Mol	Chain	Res	Type
6	A	1478	G
6	A	1481	G
6	A	1483	A
6	A	1488	G
6	A	1490	U
6	A	1501	G
6	A	1502	A
6	A	1504	G
6	A	1513	G
6	A	1514	G
7	B	4	A
7	B	9	G
7	B	11	U
7	B	12	C
7	B	13	C
7	B	30	G
7	B	42	C
7	B	57	U
7	B	58	A
7	B	59	A
7	B	67	A
7	B	87	U
7	B	89	C
7	B	90	G
7	B	103	G
7	B	107	A
7	B	114	A
58	h	7	U
58	h	9	U
58	h	12	G
58	h	20	G
58	h	31	U
58	h	48	G
58	h	55	G
58	h	60	A
58	h	68	A
58	h	71	A
58	h	72	G
58	h	82	G
58	h	89	A
58	h	90	C
58	h	94	G

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Mol	Chain	Res	Type
58	h	98	U
58	h	99	G
58	h	115	A
58	h	116	A
58	h	117	U
58	h	125	C
58	h	136	U
58	h	148	A
58	h	161	U
58	h	162	A
58	h	164	A
58	h	172	C
58	h	180	A
58	h	195	A
58	h	198	A
58	h	212	A
58	h	214	G
58	h	215	A
58	h	221	A
58	h	227	A
58	h	229	U
58	h	230	G
58	h	231	U
58	h	248	G
58	h	275	C
58	h	283	U
58	h	285	U
58	h	286	G
58	h	288	U
58	h	290	C
58	h	292	G
58	h	296	A
58	h	297	G
58	h	299	G
58	h	300	G
58	h	301	U
58	h	302	U
58	h	303	G
58	h	305	G
58	h	314	G
58	h	315	U
58	h	317	G

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Mol	Chain	Res	Type
58	h	318	U
58	h	319	G
58	h	322	A
58	h	324	C
58	h	326	A
58	h	330	U
58	h	331	U
58	h	336	C
58	h	337	U
58	h	342	C
58	h	344	G
58	h	348	G
58	h	350	A
58	h	351	G
58	h	352	G
58	h	357	U
58	h	358	G
58	h	361	A
58	h	364	A
58	h	369	G
58	h	370	U
58	h	371	G
58	h	384	G
58	h	393	U
58	h	399	G
58	h	404	A
58	h	412	A
58	h	413	G
58	h	424	G
58	h	425	U
58	h	434	G
58	h	437	G
58	h	445	U
58	h	446	G
58	h	447	A
58	h	449	G
58	h	450	G
58	h	452	G
58	h	453	U
58	h	454	U
58	h	460	G
58	h	474	G

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Mol	Chain	Res	Type
58	h	489	A
58	h	490	A
58	h	493	U
58	h	494	G
58	h	498	G
58	h	505	C
58	h	512	G
58	h	543	U
58	h	544	U
58	h	566	A
58	h	567	A
58	h	569	G
58	h	581	G
58	h	589	A
58	h	591	G
58	h	592	A
58	h	594	U
58	h	595	A
58	h	596	C
58	h	616	A
58	h	617	U
58	h	618	C
58	h	619	C
58	h	620	G
58	h	634	C
58	h	635	G
58	h	636	U
58	h	637	G
58	h	638	U
58	h	639	C
58	h	640	G
58	h	642	G
58	h	644	G
58	h	647	G
58	h	655	G
58	h	658	U
58	h	665	G
58	h	666	A
58	h	667	A
58	h	678	A
58	h	679	G
58	h	684	G

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Mol	Chain	Res	Type
58	h	685	G
58	h	696	A
58	h	706	G
58	h	707	G
58	h	708	G
58	h	721	A
58	h	728	G
58	h	731	A
58	h	738	A
58	h	740	A
58	h	756	A
58	h	758	A
58	h	760	U
58	h	764	U
58	h	765	G
58	h	766	G
58	h	768	G
58	h	784	G
58	h	785	A
58	h	794	G
58	h	801	U
58	h	845	C
58	h	855	C
58	h	862	U
58	h	863	G
58	h	868	C
58	h	872	G
58	h	878	G
58	h	879	A
58	h	880	G
58	h	890	G
58	h	891	G
58	h	897	A
58	h	899	G
58	h	904	A
58	h	907	A
58	h	917	A
58	h	920	G
58	h	927	C
58	h	942	U
58	h	944	A
58	h	960	G

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Mol	Chain	Res	Type
58	h	961	U
58	h	972	A
58	h	974	G
58	h	975	U
58	h	981	U
58	h	982	A
58	h	994	A
58	h	1001	C
58	h	1002	C
58	h	1003	A
58	h	1004	C
58	h	1005	A
58	h	1006	G
58	h	1007	G
58	h	1008	G
58	h	1011	A
58	h	1013	U
58	h	1014	G
58	h	1020	A
58	h	1022	C
58	h	1025	A
58	h	1046	C
58	h	1047	A
58	h	1048	A
58	h	1049	G
58	h	1058	A
58	h	1063	G
58	h	1076	A
58	h	1078	G
58	h	1085	G
58	h	1092	G
58	h	1101	A
58	h	1103	C
58	h	1114	G
58	h	1130	C
58	h	1131	G
58	h	1144	A
58	h	1151	U
58	h	1164	A
58	h	1171	C
58	h	1173	G
58	h	1175	A

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Mol	Chain	Res	Type
58	h	1178	U
58	h	1181	G
58	h	1184	U
58	h	1186	G
58	h	1187	A
58	h	1188	A
58	h	1189	G
58	h	1190	C
58	h	1191	A
58	h	1201	G
58	h	1202	A
58	h	1203	A
58	h	1205	G
58	h	1206	A
58	h	1207	G
58	h	1209	G
58	h	1212	U
58	h	1213	A
58	h	1214	A
58	h	1219	U
58	h	1230	G
58	h	1232	G
58	h	1240	G
58	h	1250	U
58	h	1251	A
58	h	1253	C
58	h	1254	G
58	h	1260	C
58	h	1261	A
58	h	1292	U
58	h	1293	G
58	h	1298	C
58	h	1335	G
58	h	1344	A
58	h	1353	G
58	h	1362	A
58	h	1365	G
58	h	1371	G
58	h	1386	G
58	h	1387	A
58	h	1389	U
58	h	1404	C

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Mol	Chain	Res	Type
58	h	1415	A
58	h	1416	A
58	h	1435	C
58	h	1436	C
58	h	1437	A
58	h	1448	C
58	h	1456	G
58	h	1465	C
58	h	1467	U
58	h	1480	A
58	h	1494	U
58	h	1499	A
58	h	1502	G
58	h	1507	G
58	h	1508	A
58	h	1510	A
58	h	1522	G
58	h	1529	U
58	h	1531	C
58	h	1532	G
58	h	1533	U
58	h	1534	C
58	h	1536	A
58	h	1540	U
58	h	1549	G
58	h	1550	G
58	h	1551	U
58	h	1552	A
58	h	1553	C
58	h	1625	G
58	h	1629	G
58	h	1630	U
58	h	1632	G
58	h	1639	G
58	h	1640	A
58	h	1641	U
58	h	1648	A
58	h	1649	C
58	h	1670	G
58	h	1676	G
58	h	1679	A
58	h	1680	A

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Mol	Chain	Res	Type
58	h	1681	U
58	h	1703	G
58	h	1711	G
58	h	1713	U
58	h	1714	A
58	h	1715	A
58	h	1716	A
58	h	1717	U
58	h	1724	G
58	h	1728	U
58	h	1731	A
58	h	1737	A
58	h	1738	G
58	h	1754	G
58	h	1755	A
58	h	1756	G
58	h	1757	U
58	h	1767	U
58	h	1768	C
58	h	1769	G
58	h	1786	G
58	h	1789	A
58	h	1798	U
58	h	1801	C
58	h	1802	G
58	h	1803	A
58	h	1826	A
58	h	1844	A
58	h	1864	U
58	h	1866	C
58	h	1867	G
58	h	1870	U
58	h	1871	G
58	h	1872	A
58	h	1892	G
58	h	1893	C
58	h	1895	A
58	h	1946	U
58	h	1947	U
58	h	1949	C
58	h	1950	G
58	h	1973	C

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Mol	Chain	Res	Type
58	h	1974	A
58	h	1975	A
58	h	1981	U
58	h	1990	A
58	h	2001	A
58	h	2017	C
58	h	2018	G
58	h	2026	A
58	h	2033	U
58	h	2046	A
58	h	2064	A
58	h	2065	A
58	h	2074	G
58	h	2075	G
58	h	2085	C
58	h	2086	U
58	h	2088	C
58	h	2089	C
58	h	2090	U
58	h	2091	U
58	h	2092	U
58	h	2093	G
58	h	2094	G
58	h	2095	G
58	h	2096	G
58	h	2107	G
58	h	2110	U
58	h	2111	U
58	h	2112	U
58	h	2125	A
58	h	2129	C
58	h	2130	G
58	h	2137	A
58	h	2138	C
58	h	2140	A
58	h	2141	U
58	h	2153	G
58	h	2154	G
58	h	2160	A
58	h	2162	A
58	h	2163	U
58	h	2179	U

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Mol	Chain	Res	Type
58	h	2184	A
58	h	2189	C
58	h	2190	A
58	h	2191	C
58	h	2194	A
58	h	2195	U
58	h	2196	G
58	h	2215	U
58	h	2217	U
58	h	2221	A
58	h	2244	A
58	h	2247	A
58	h	2255	A
58	h	2256	G
58	h	2257	A
58	h	2263	G
58	h	2267	C
58	h	2276	G
58	h	2279	C
58	h	2280	G
58	h	2284	A
58	h	2285	G
58	h	2286	A
58	h	2316	G
58	h	2320	C
58	h	2324	A
58	h	2325	U
58	h	2329	G
58	h	2330	U
58	h	2331	U
58	h	2333	G
58	h	2334	U
58	h	2335	G
58	h	2336	U
58	h	2337	A
58	h	2338	G
58	h	2339	G
58	h	2340	A
58	h	2341	U
58	h	2342	A
58	h	2343	G
58	h	2346	G

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Mol	Chain	Res	Type
58	h	2349	A
58	h	2351	A
58	h	2354	G
58	h	2355	U
58	h	2356	G
58	h	2357	A
58	h	2368	C
58	h	2380	G
58	h	2382	G
58	h	2384	C
58	h	2385	G
58	h	2386	U
58	h	2387	U
58	h	2388	G
58	h	2393	A
58	h	2394	A
58	h	2395	U
58	h	2396	A
58	h	2400	C
58	h	2401	U
58	h	2402	C
58	h	2407	C
58	h	2413	G
58	h	2421	A
58	h	2427	G
58	h	2430	C
58	h	2434	A
58	h	2436	A
58	h	2449	A
58	h	2462	G
58	h	2463	G
58	h	2467	U
58	h	2507	C
58	h	2511	A
58	h	2512	A
58	h	2528	G
58	h	2529	A
58	h	2531	G
58	h	2532	G
58	h	2533	C
58	h	2548	U
58	h	2549	G

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Mol	Chain	Res	Type
58	h	2559	A
58	h	2569	G
58	h	2571	C
58	h	2574	C
58	h	2581	G
58	h	2607	G
58	h	2609	A
58	h	2615	G
58	h	2627	C
58	h	2631	G
58	h	2640	G
58	h	2647	U
58	h	2649	A
58	h	2653	G
58	h	2654	A
58	h	2655	U
58	h	2659	A
58	h	2665	C
58	h	2672	A
58	h	2677	A
58	h	2688	C
58	h	2693	A
58	h	2694	G
58	h	2698	C
58	h	2699	C
58	h	2700	A
58	h	2702	A
58	h	2705	G
58	h	2715	U
58	h	2718	G
58	h	2722	C
58	h	2726	G
58	h	2729	G
58	h	2742	A
58	h	2744	C
58	h	2749	G
58	h	2753	G
58	h	2759	G
58	h	2786	U
58	h	2790	A
58	h	2791	G
58	h	2796	A

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Mol	Chain	Res	Type
58	h	2797	C
58	h	2826	A
58	h	2827	G
58	h	2833	U
58	h	2837	U
58	h	2839	U
58	h	2853	C
58	h	2854	A
58	h	2862	G
58	h	2865	G
58	h	2870	C
58	h	2876	C
58	h	2878	A
58	h	2909	G
58	h	2913	U
58	h	2915	C
58	h	2926	A
58	h	2936	C
58	h	2938	G
58	h	2940	U
58	h	2948	C
58	h	2950	C
58	h	2957	A
58	h	2968	G
58	h	2972	A
58	h	2982	A
58	h	2985	G
58	h	3002	A
58	h	3009	U
58	h	3014	A
58	h	3015	C
58	h	3020	U
58	h	3021	A
58	h	3022	G
58	h	3041	C
58	h	3042	A
58	h	3056	A
58	h	3082	U
58	h	3088	C
58	h	3093	A
58	h	3101	C
58	h	3105	C

Continued on next page...

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Mol	Chain	Res	Type
58	h	3106	C
58	h	3114	A

All (13) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	4	18	G
6	A	92	A
6	A	422	C
6	A	429	U
6	A	485	G
6	A	498	C
6	A	895	A
6	A	1007	U
6	A	1117	U
6	A	1149	C
6	A	1477	A
6	A	1482	U
7	B	10	G

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 18 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
60	GNP	7	801	-	34,34,34	1.29	5 (14%)	47,54,54	0.64	0
59	PHE	2	101	-	10,11,12	0.39	0	8,13,15	0.17	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	GNP	7	801	-	-	5/18/38/38	0/3/3/3
59	PHE	2	101	-	-	1/5/6/8	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	7	801	GNP	PB-O3A	4.37	1.64	1.59
60	7	801	GNP	PB-O1B	3.12	1.50	1.46
60	7	801	GNP	PG-N3B	3.02	1.71	1.63
60	7	801	GNP	PG-O1G	2.86	1.50	1.46
60	7	801	GNP	PB-O2B	-2.28	1.50	1.56

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	2	101	PHE	O-C-CA-CB
60	7	801	GNP	PG-N3B-PB-O1B
60	7	801	GNP	O4'-C4'-C5'-O5'
60	7	801	GNP	C3'-C4'-C5'-O5'
60	7	801	GNP	C4'-C5'-O5'-PA
60	7	801	GNP	PB-O3A-PA-O1A

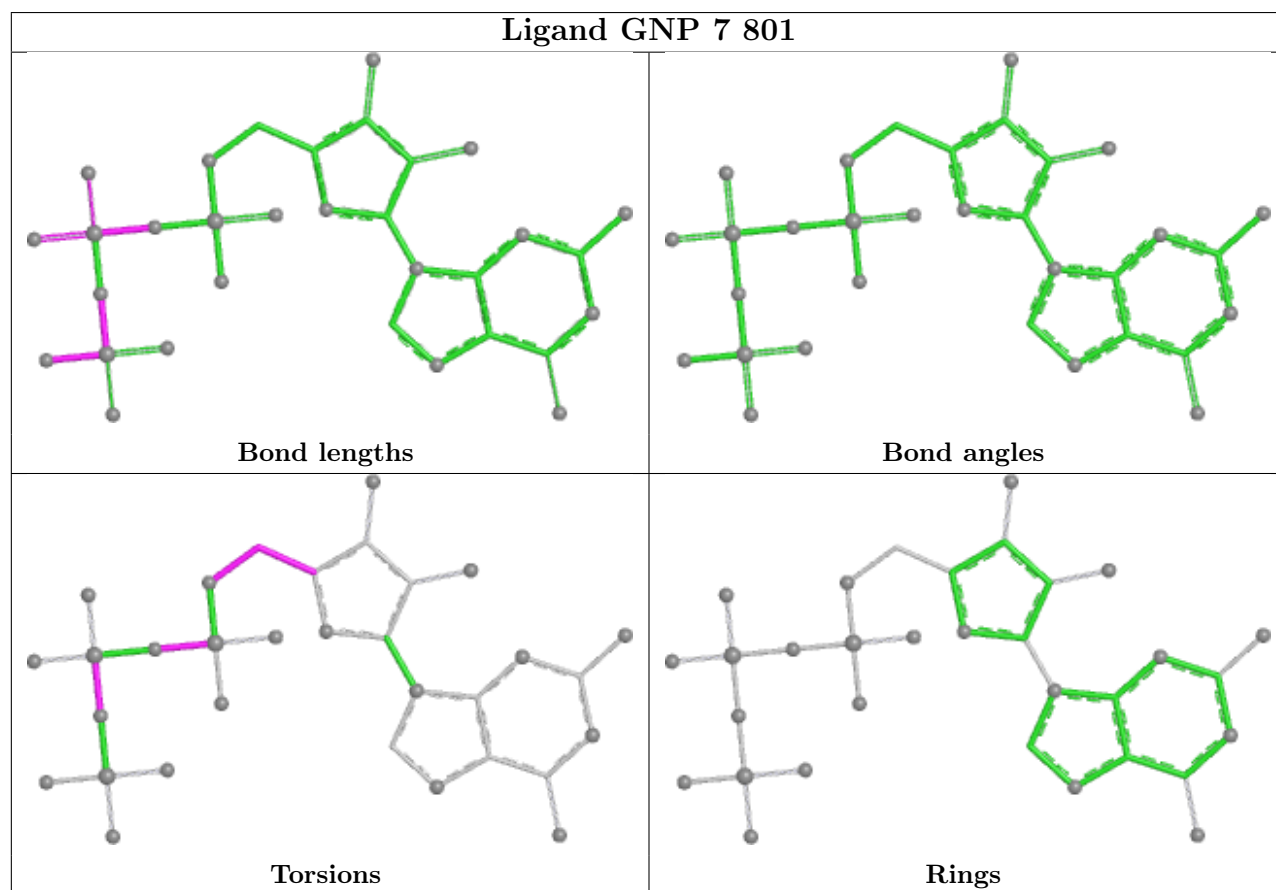
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	7	801	GNP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

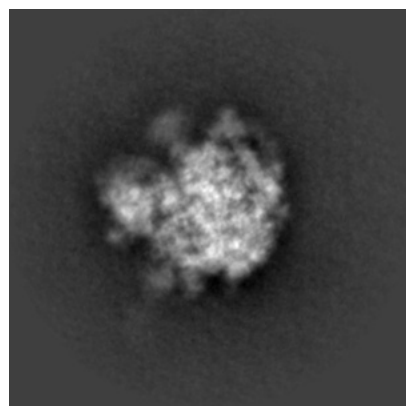
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61959. These allow visual inspection of the internal detail of the map and identification of artifacts.

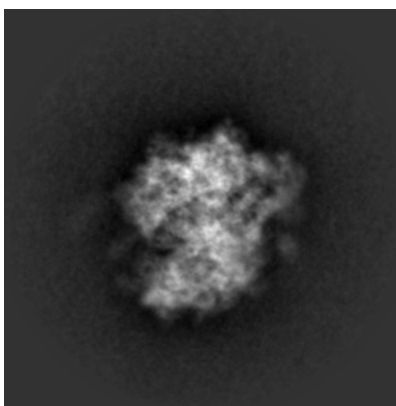
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

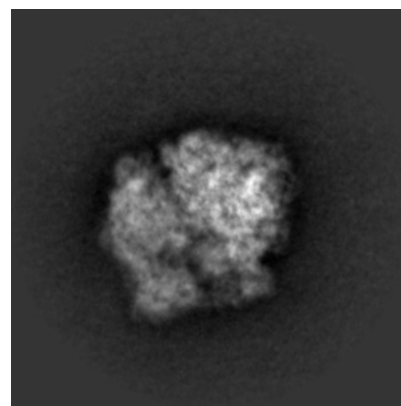
6.1.1 Primary map



X

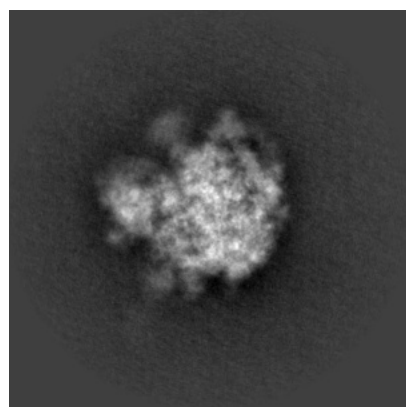


Y

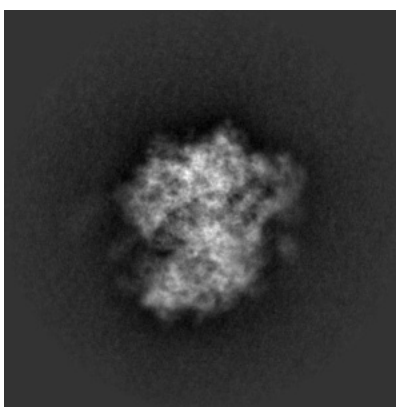


Z

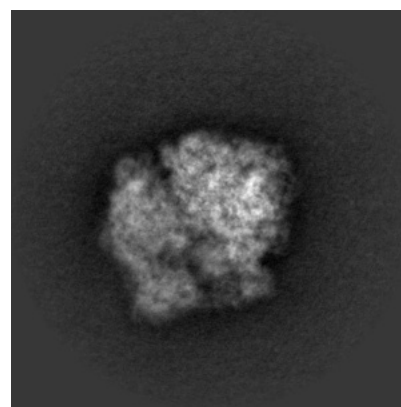
6.1.2 Raw map



X



Y

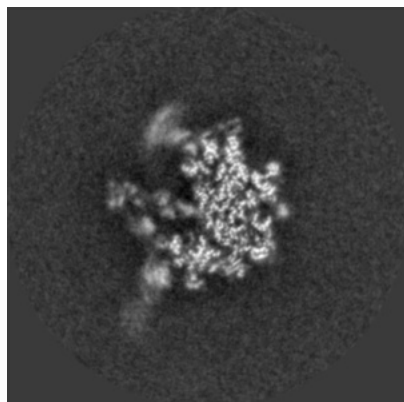


Z

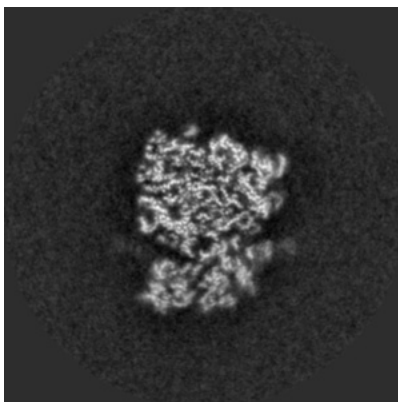
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

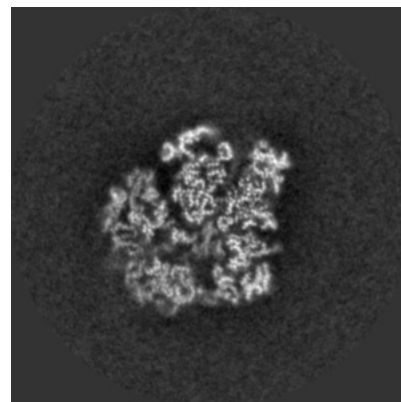
6.2.1 Primary map



X Index: 175

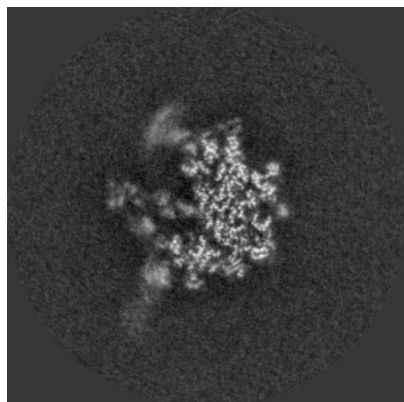


Y Index: 175

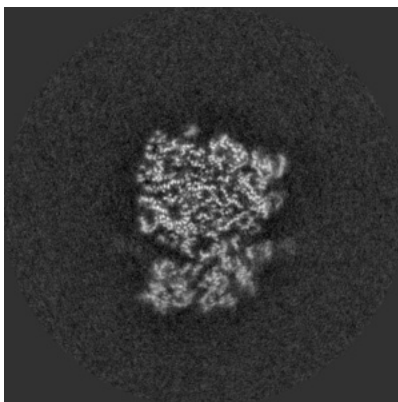


Z Index: 175

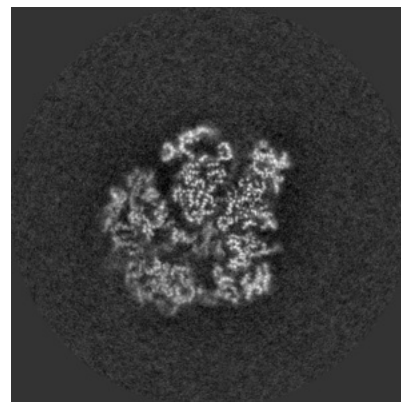
6.2.2 Raw map



X Index: 175



Y Index: 175

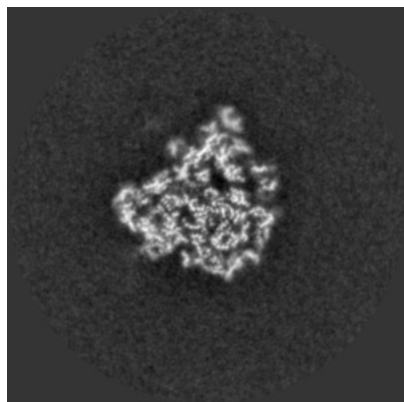


Z Index: 175

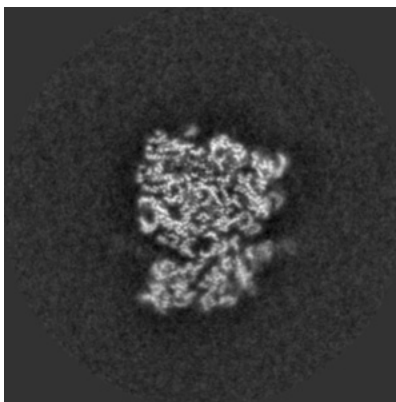
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

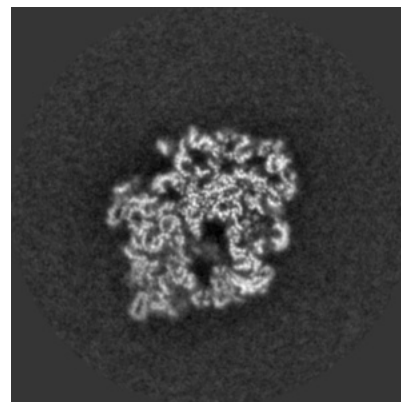
6.3.1 Primary map



X Index: 210

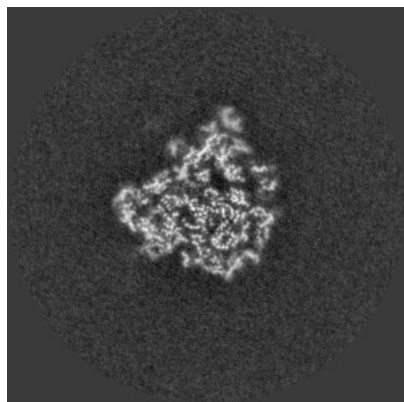


Y Index: 176

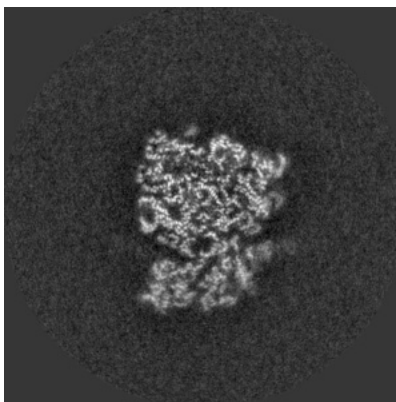


Z Index: 188

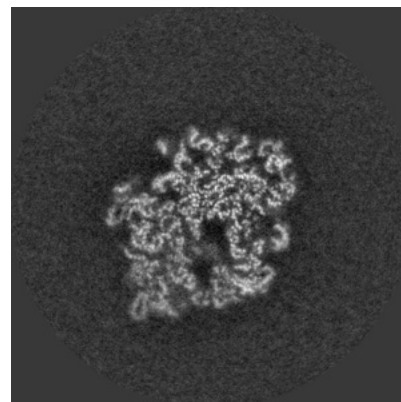
6.3.2 Raw map



X Index: 210



Y Index: 176

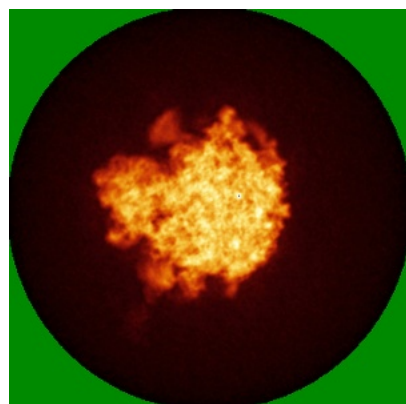


Z Index: 187

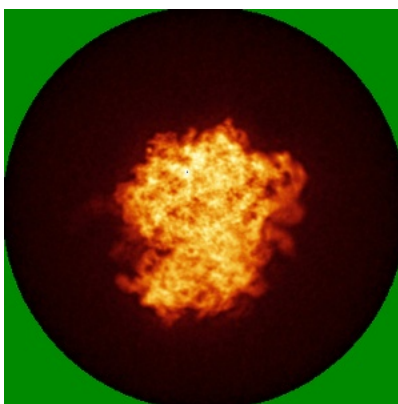
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

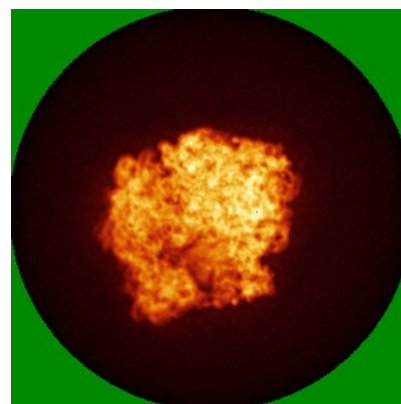
6.4.1 Primary map



X

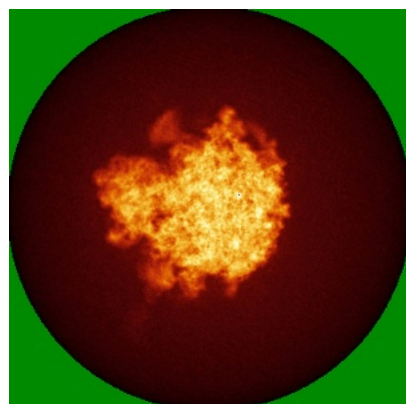


Y

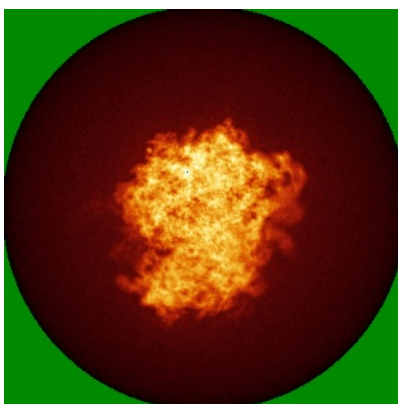


Z

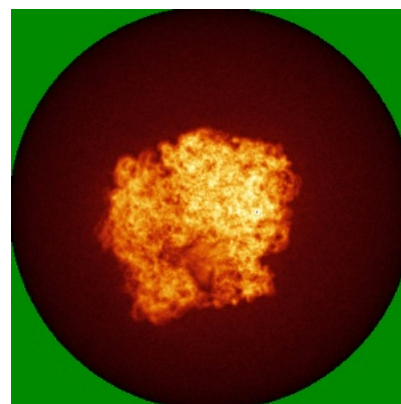
6.4.2 Raw map



X



Y

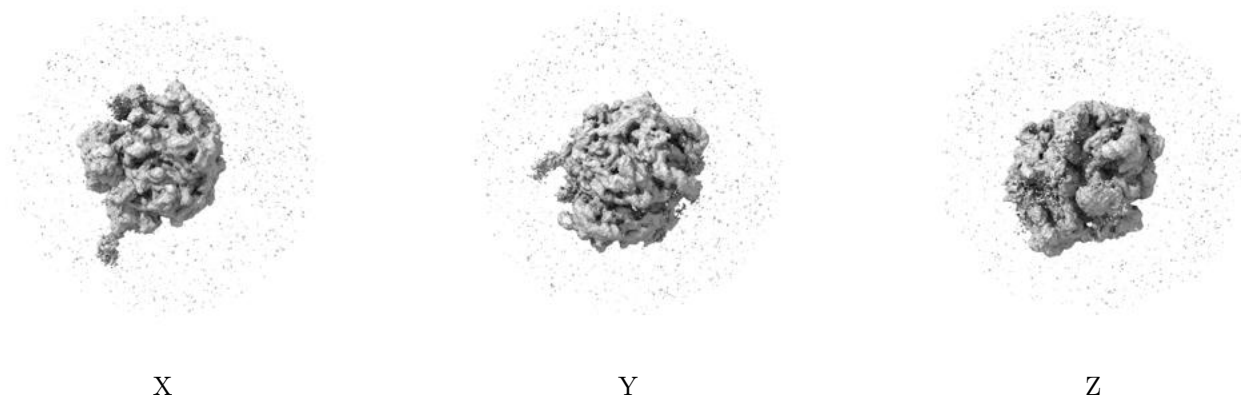


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

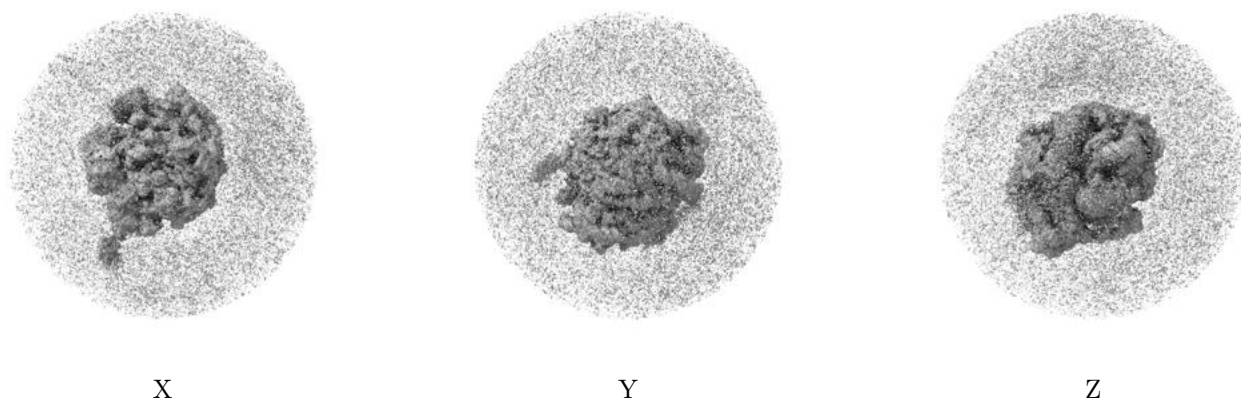
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00715. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

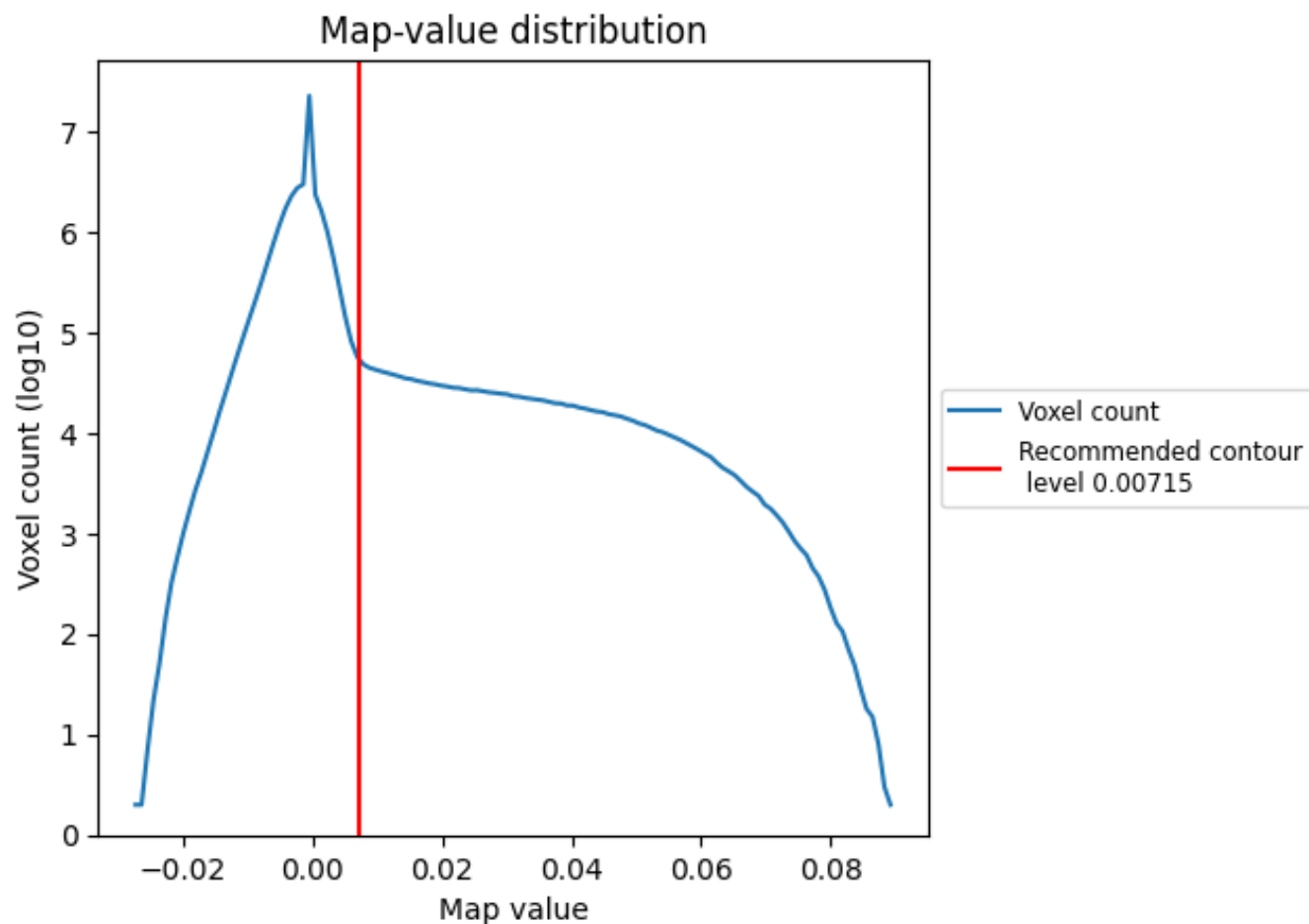
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

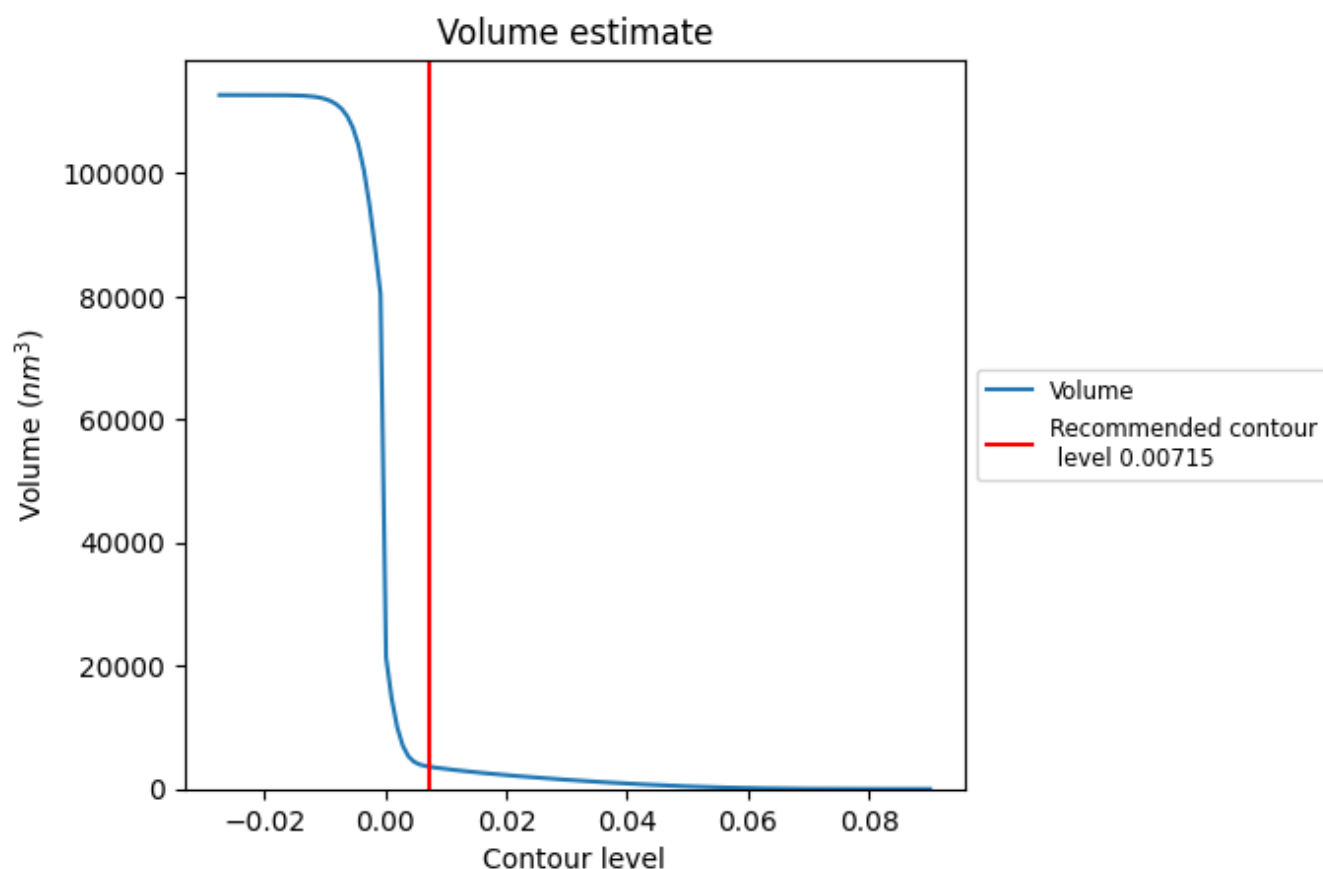
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

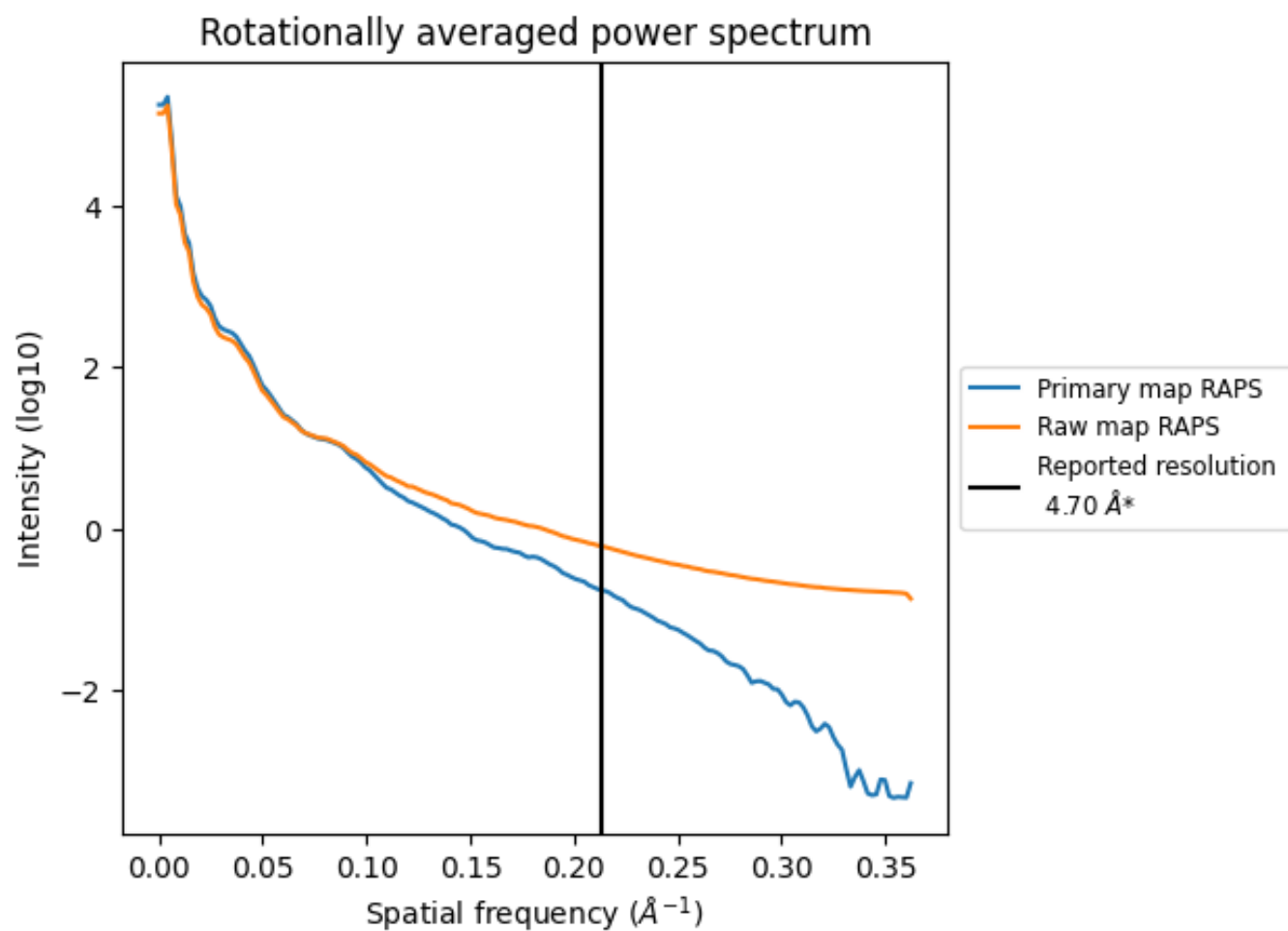
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3647 nm^3 ; this corresponds to an approximate mass of 3295 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

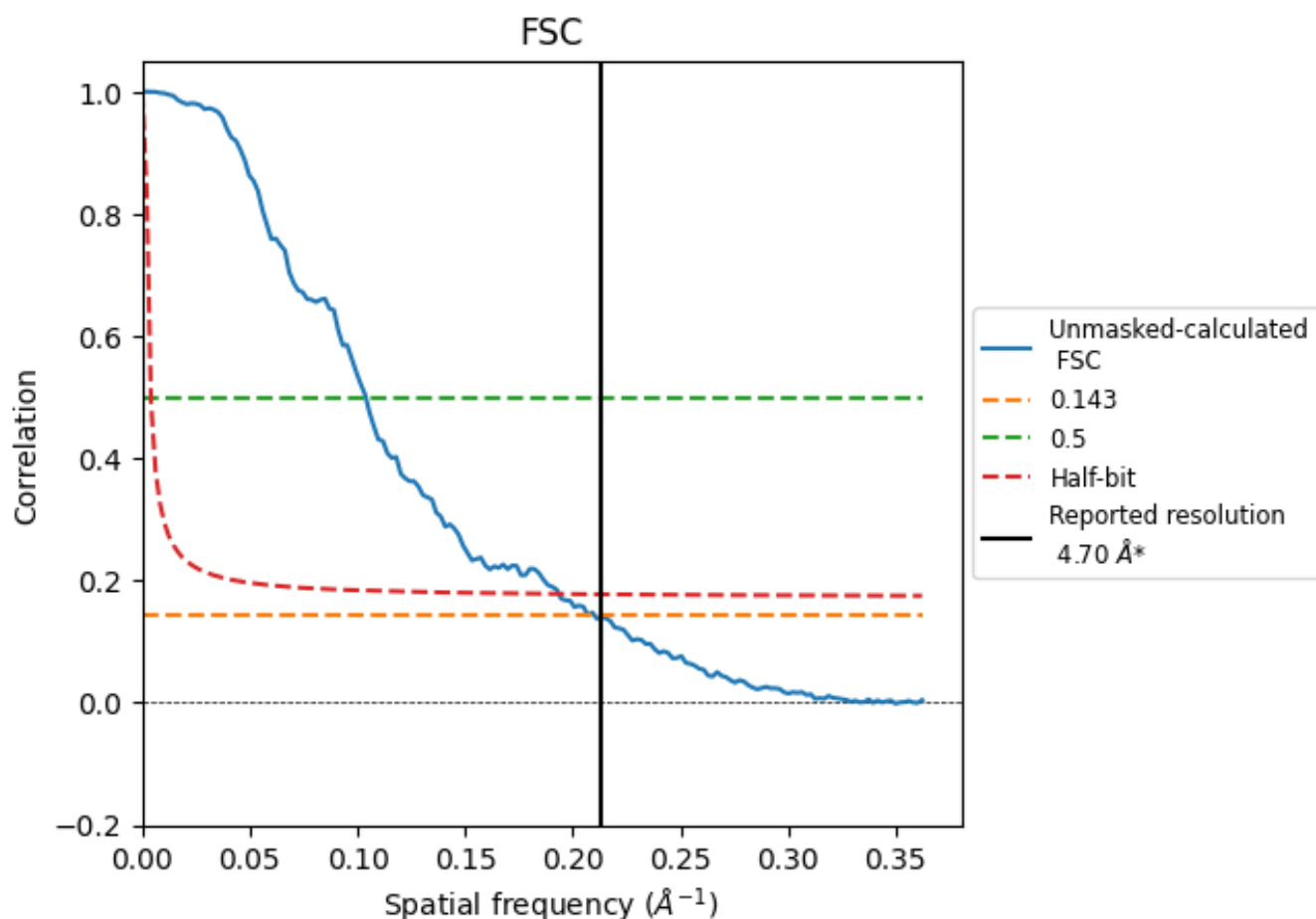


*Reported resolution corresponds to spatial frequency of 0.213 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.213 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

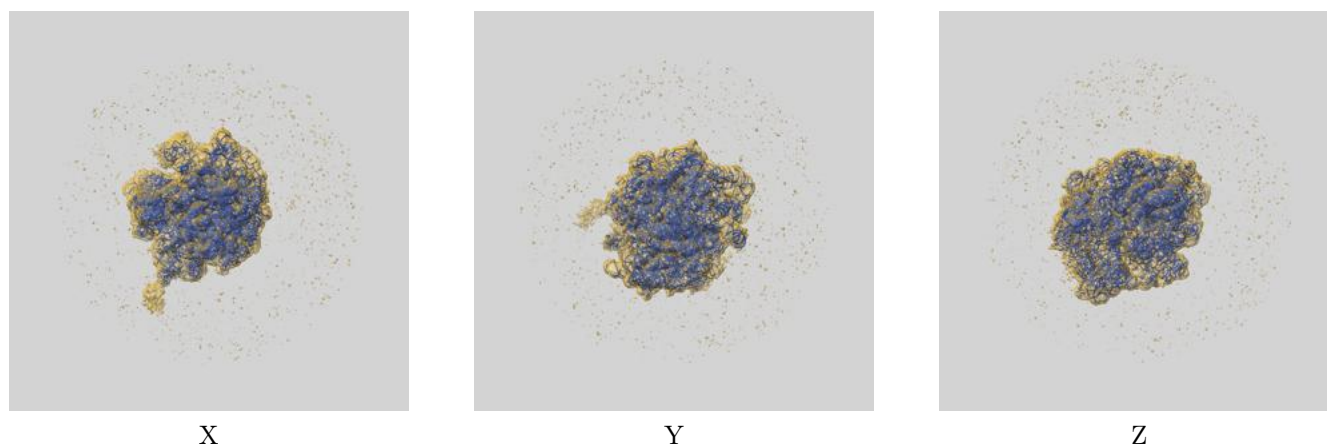
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.83	9.63	5.17

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

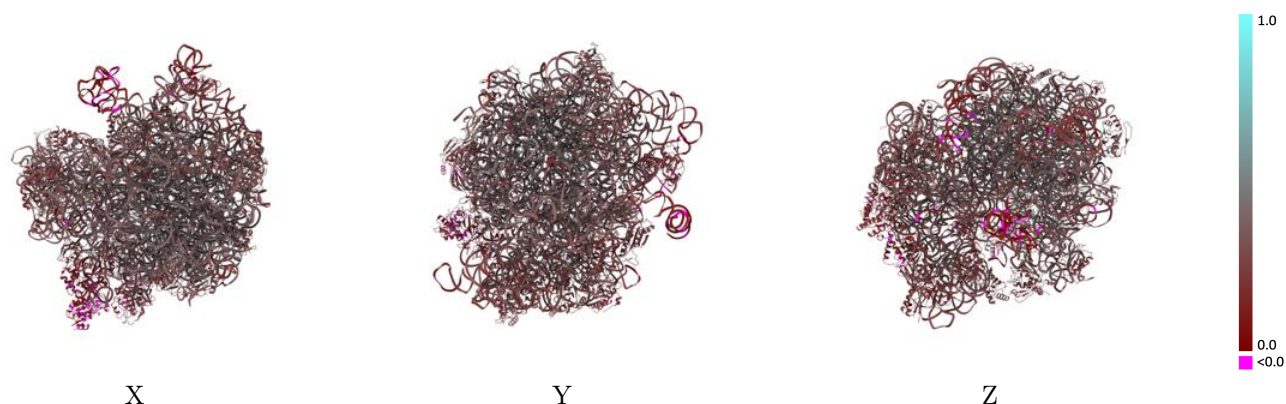
This section contains information regarding the fit between EMDB map EMD-61959 and PDB model 9K0Z. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



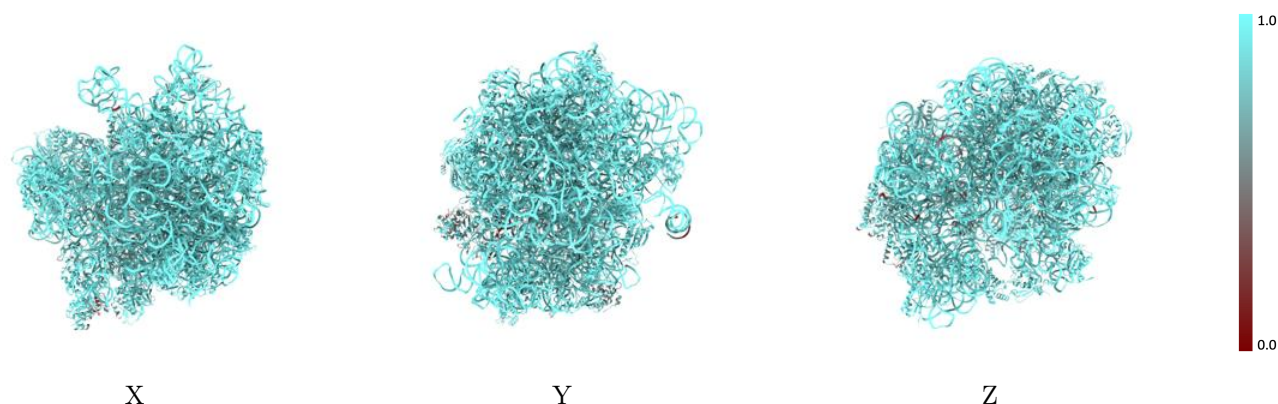
The images above show the 3D surface view of the map at the recommended contour level 0.00715 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



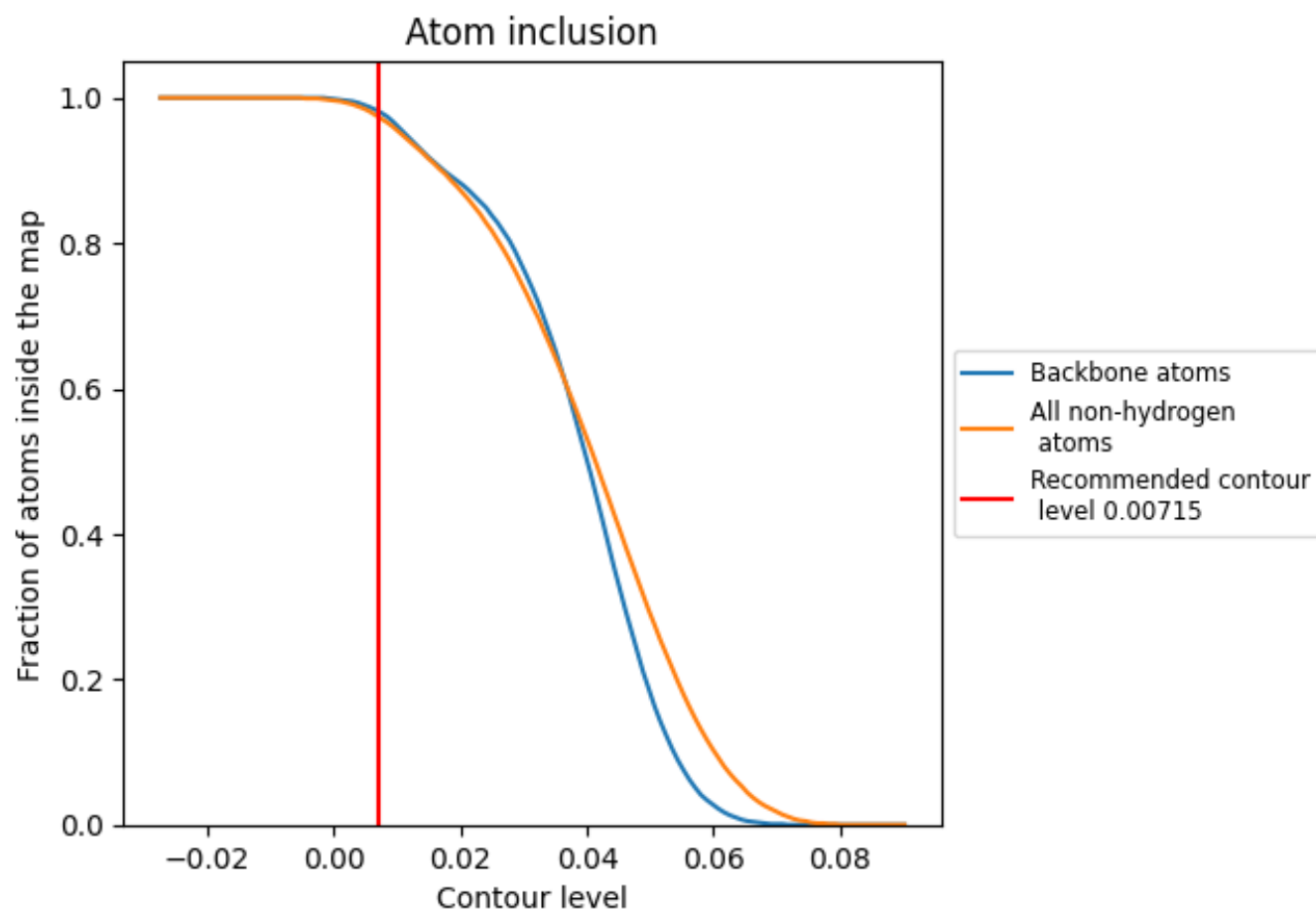
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00715).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.00715) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9730	 0.3180
1	 0.9880	 0.2940
2	 0.9910	 0.3160
3	 0.9940	 0.3320
4	 0.9180	 0.1900
5	 0.3080	 0.0730
7	 0.6530	 0.1680
A	 0.9990	 0.3140
B	 0.9990	 0.3430
C	 0.9790	 0.2540
D	 0.9850	 0.2430
E	 0.9570	 0.2700
F	 0.9550	 0.2750
G	 0.9780	 0.2500
H	 0.9920	 0.2790
I	 0.9970	 0.2400
J	 0.9920	 0.2580
K	 0.9920	 0.2920
L	 0.9580	 0.2980
M	 0.9930	 0.2600
N	 0.9890	 0.2880
O	 0.9630	 0.2720
P	 0.9700	 0.2650
Q	 0.9630	 0.2720
R	 0.9960	 0.2770
S	 0.9880	 0.2570
T	 0.9560	 0.2300
U	 0.9850	 0.3260
V	 0.7190	 0.1700
W	 0.8560	 0.2780
X	 0.9980	 0.3770
Y	 0.9910	 0.3660
Z	 0.9960	 0.2740
a	 0.9870	 0.3390
b	 0.9880	 0.3750



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Chain	Atom inclusion	Q-score
c	 0.9620	 0.3280
d	 0.9860	 0.3590
e	 0.8790	 0.2660
f	 0.9970	 0.3430
g	 0.9970	 0.2760
h	 0.9960	 0.3540
i	 0.9760	 0.3580
j	 0.9940	 0.3700
k	 0.9860	 0.3490
l	 0.9890	 0.2730
m	 0.9860	 0.2940
n	 0.9410	 0.2660
o	 0.9000	 0.0890
p	 0.9690	 0.1050
q	 0.9870	 0.3570
r	 0.9770	 0.3520
s	 0.9950	 0.3370
t	 0.9860	 0.3660
u	 0.9890	 0.3480
v	 0.9960	 0.3020
w	 0.9770	 0.3520
x	 0.9920	 0.3360
y	 0.9950	 0.3840
z	 0.9880	 0.3700